



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 179985

TO: Sheridan Swope
Location: REM-2B71&3C60
Art Unit: 1656
Wednesday, February 22, 2006
Case Serial Number: 10/617443

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Examiner Swope,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
X22523

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STIC-Biotech/ChemLib

179986

From: Chan, Christina
Sent: Tuesday, February 21, 2006 12:56 PM
To: Swope, Sheridan; STIC-Biotech/ChemLib
Subject: RE: 10/617,443

~~Please rush.~~ Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

CRFL

-----Original Message-----

From: Swope, Sheridan
Sent: Tuesday, February 21, 2006 12:11 PM
To: Chan, Christina
Subject: 10/617,443

Chris, May I have this rushed for an AF allowance?

For 10/617,443, pls interference search only:

SID 1 against the NT and AA databases.

SID 2 against the NT and AA databases.

Thanks,

Sheridan Swope, Ph.D.
Patent Examiner, AU 1656
Recombinant Enzymes
571-272-0943 (voice)
E02B71 Remsen Bld (Office)
E03C70 Remsen Bld (Mailbox)

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 21, 2006, 18:07:50 ; Search time 512 Seconds
(without alignments) 10436.231 Million cell updates/sec

Title: US-10-617-443b-1

Perfect score: 3006

Sequence: 1 caggagactcgaggttcgag.....gcccaaaaaaaaaaaaaa 3006

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/1_COMB_seq:*
- 2: /cgn2_6/prodata/1/ina/5_COMB_seq:*
- 3: /cgn2_6/prodata/1/ina/6A_COMB_seq:*
- 4: /cgn2_6/prodata/1/ina/6B_COMB_seq:*
- 5: /cgn2_6/prodata/1/ina/H_COMB_seq:*
- 6: /cgn2_6/prodata/1/ina/PCTUS_COMB_seq:*
- 7: /cgn2_6/prodata/1/ina/PP_COMB_seq:*
- 8: /cgn2_6/prodata/1/ina/RE_COMB_seq:*
- 9: /cgn2_6/prodata/1/ina/backfilest1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	385	12.8	1894	3	US-10-104-047-795 Sequence 795, App
2	385	12.8	2036	3	US-09-949-016-339 Sequence 399, App
3	384.6	12.8	2036	3	US-08-923-454A-17 Sequence 17, App1
4	383.4	12.8	2205	3	US-08-888-077A-41 Sequence 41, App1
5	383	12.7	1521	3	US-09-949-016-4643 Sequence 4643, Ap
6	322.8	10.7	1859	3	US-09-724-864-22 Sequence 22, App1
7	290.6	9.7	1835	3	US-08-923-454A-7 Sequence 7, App1
8	290.6	9.7	2040	3	US-09-075-460-4 Sequence 4, App1
9	290.6	9.7	2187	3	US-08-923-454A-23 Sequence 23, App1
10	290.6	9.7	2187	3	US-08-923-454A-24 Sequence 24, App1
11	290.6	9.7	2476	3	US-09-008-271A-23 Sequence 23, App1
12	290.6	9.7	2476	3	US-09-968-415-23 Sequence 23, App1
13	289	9.6	2187	3	US-08-923-454A-30 Sequence 30, App1
14	227	7.6	539	2	US-08-322-742-18 Sequence 18, App1
15	217.8	7.2	1503	3	US-08-923-454A-5 Sequence 5, App1
16	217.8	7.2	2144	3	US-08-923-454A-28 Sequence 28, App1
17	208	6.9	1787	3	US-08-923-454A-3 Sequence 3, App1
18	208	6.9	2551	3	US-08-923-454A-26 Sequence 26, App1
19	128.2	4.3	3006	3	US-09-949-016-1241 Sequence 1241, A
20	128.2	4.3	57299	3	US-09-949-016-1241 Sequence 1241, A
21	125.4	4.2	732	3	US-08-923-454A-1 Sequence 1, App1
22	121.8	4.1	1332	3	US-09-902-540-4672 Sequence 4672, Ap
23	121.8	4.1	24754	3	US-09-902-540-1230 Sequence 1230, Ap
24	112.8	3.8	1260	3	US-09-902-540-8673 Sequence 8673, Ap

c	25	112.8	3.8	9191	3	US-09-902-540-918	Sequence 918, App
	26	112.6	3.7	1771	3	US-08-818-112-13	Sequence 13, App1
	27	112.6	3.7	1771	3	US-08-818-111-13	Sequence 13, App1
	28	112.6	3.7	1771	3	US-09-056-556-13	Sequence 13, App1
	29	112.6	3.7	1771	3	US-09-072-596-13	Sequence 13, App1
	30	112.6	3.7	1771	3	US-09-072-596-13	Sequence 13, App1
	31	112.6	3.7	1771	3	US-10-193-002-13	Sequence 13, App1
	32	112.6	3.7	1771	3	US-10-084-844-13	Sequence 13, App1
	33	112.6	3.7	4403765	3	US-09-103-840A-2	Sequence 2, App1
	34	112.6	3.7	4411529	3	US-09-103-840A-1	Sequence 1, App1
	35	109.6	3.6	1195	3	US-09-712-363-36	Sequence 36, App1
	36	106.8	3.6	1224	3	US-09-252-991A-9171	Sequence 8171, Ap
c	37	106.8	3.6	1380	3	US-09-252-991A-7981	Sequence 7981, Ap
	38	102.6	3.4	1650	3	US-09-712-363-44	Sequence 44, App1
	39	102	3.4	1167	3	US-09-902-540-5297	Sequence 5297, Ap
c	40	102	3.4	30783	3	US-09-902-540-1258	Sequence 1258, Ap
	41	101	3.4	38675	3	US-08-311-731A-135	Sequence 135, App
c	42	100.2	3.3	1488	3	US-09-489-039A-5255	Sequence 5255, Ap
	43	100.2	3.3	1494	3	US-09-489-039A-5193	Sequence 5193, Ap
	44	100	3.3	495	3	US-09-702-705-897	Sequence 897, App
	45	100	3.3	495	3	US-09-736-457-897	Sequence 897, App

ALIGNMENTS

RESULT 1									
US-10-104-047-795									
; Sequence 795, Application US/10104047									
; Patent No. 6943241									
; GENERAL INFORMATION:									
; APPLICANT: HELIX RESEARCH INSTITUTE									
; TITLE OF INVENTION: NO. 6943241el full length cDNA									
; FILE REFERENCE: H1-A0105									
; CURRENT APPLICATION NUMBER: US/10/104.047									
; PRIOR FILING DATE: 2002-03-25									
; PRIOR APPLICATION NUMBER:									
; NUMBER OF SEQ ID NOS: 4096									
; SOFTWARE: PatentIn Ver. 2.1									
; SEQ ID NO 795									
; LENGTH: 1894									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-10-104-047-795									
Query Match									
Best Local Similarity 63.8%; Pred. No. 6.7e-83;									
Matches 630; Conservative									
Score 385; DB 3; Length 1894;									
Pred. No. 6.7e-83;									
Matches 630; Indels 27; Gaps 2;									
QY	1027	CGCCAGCGCAGGTTCCACGCTGAGCAGCCCGCTCAAGTTCACCTTCATTGCTG	1086						
DB	364	CTTGCGGCGCAGGCGAGAGATCCCAAGTTGCGCATTAATTAATTAATTCGCGG	423						
QY	1087	ACGTGTGGAAGAATGCGACCGCGGTGTCATCATGAGTCTTCTGAGACACCGC	1146						
DB	424	ACGTGTGGAAGAATGCGACCGCGGTGTCATCATGAGTCTTCTGAGACACCGC	483						
QY	1147	TGTTGGCGCGCAACGTGCGCCCTGTCACGCGTTCTGCTTCATCATGTCAGAGCGCGC	1206						
DB	484	TTTCTAAACGAGAGGTGCGCGGTGCTAGAGGTTTATGTTGTCGGAAGTGAAC	543						
QY	1207	TGATCATCACCATGCGCCAGCTGTGTGTCAGCAAGTGTGCCCCGGGCGAGCAGC	1266						
DB	544	TGATGTGTCACCAATGCCACGCTGTGTCAGCAACAA-----GCACCGGG	585						
QY	1267	TCAAGTGAGTACAGATGGGAGCTCTTATGAGCCCAACCATCAAGATCGACAAGA	1326						
DB	586	TCAAGTGAGTACAGATGGGAGCTCTTATGAGCCCAACCATCAAGATCGACAAGA	645						
QY	1327	ACTCGACATTCGACCATCAAGATCATCCCAAGAAAAGCTCCCTGTGTGTTGCTGG	1386						
DB	646	AAGCAGATCGACCATCAAGATCATCCCAAGAAAAGCTCCCTGTGTGTTGCTGG	705						

QY 1387 GTCACCTGGCGGACCTGCGGCTGGGGAGTTTGTGTGGCCATCGGCAATCCCTTGGCCC 1446
DB 706 GCCGCTCTCAGAGCTCGGCGCGGAGAGTTTGTGTGGCCATCGGCAATCCCTTGGCCC 765
QY 1447 TACAGAACACAGTGAACACCGGCACTGTCAGCACTGCGGAGGAGGAGGAGCTGG 1506
DB 766 TTCAAAACACAGTGAACACCGGCACTGTCAGCACTGCGGAGGAGGAGGAGCTGG 825
QY 1507 GCCTCCGGGAGCTCGGAGTGAATGATTCAGTGAATGATTCAGTGAATGATTCAGTGAAT 1566
DB 826 GGCCTCGGCACTGAGATGATGATTCAGTGAATGATTCAGTGAATGATTCAGTGAAT 885
QY 1567 CCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1626
DB 886 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 945
QY 1627 CGGCTGGCATCTCTTGGCATCTCTTGGCATCTCTTGGCATCTCTTGGCATCTCTTGG 1686
DB 946 CAGCTGGATCTCTTGGCATCTCTTGGCATCTCTTGGCATCTCTTGGCATCTCTTGG 1005
QY 1687 AAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1737
DB 1006 ATGACGAGCAGGCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1065
QY 1738 GAGCAGTACACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1797
DB 1066 TGTACCTACGTCAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1125
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DB 1126 TGATCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1185
QY 1858 TCAAGATGATGATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1917
DB 1186 TCAAGAGAAACGAGTATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1245
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QY 1978 ACCTCTCTTTCAGCATGCGACCTGAGG 2004
DB 1306 ATATCATGATCAGATGATTCGCGAAG 1332

RESULT 2

US-09-949-016-399
; Sequence 399, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 399
; LENGTH: 2036
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-399

Query Match 12.8%; Score 385; DB 3; Length 2036;
Best Local Similarity 63.8%; Pred. No. 6; 9e-83;

Matches 630; Conservative 0; Mismatches 330; Indels 27; Gaps 2;

QY 1027 CCGCCAGCGCAGATCTCCACAGCTGAGAGCGCCGCGTACAGAGTTCAATTCATTCTG 1086
DB 509 CCGCGGCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 568
QY 1087 ACGTGTGAGAGAGATTCGACAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1146
DB 569 ACGTGTGAGAGAGATTCGACAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 628
QY 1147 TGTGTGGCGCAAGCTGCGCTGTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1206
DB 629 TTTCTTAAACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 688
QY 1207 TGATCATCAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1266
DB 689 TGATCATCAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 730
QY 1267 TCAAGGTGAGCTTACAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1326
DB 731 TCAAGGTGAGCTTACAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 790
QY 1327 AGTGGAGATTCGACACATCAAGATTCATCCCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1386
DB 791 AAGCAGACATCGACATCAAAATTTGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 850
QY 1387 GTCACCTGGCGGACCTGCGGCTGGGGAGTTTGTGTGGCCATCGGCAATCCCTTGGCCC 1446
DB 851 GCCGCTCTCAGAGCTCGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 910
QY 1447 TACAGAACACAGTGAACACCGGCACTGTCAGCACTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1506
DB 911 TTCAAAACACAGTGAACACCGGCACTGTCAGCACTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 970
QY 1507 GCCTCCGGGAGCTCGACATGATGATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1566
DB 971 GGCCTCGGCACTGACATGATGATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1030
QY 1567 CCGGGGAG 1626
DB 1031 CCGGAG 1090
QY 1627 CGGCTGGCATCTCTTGGCATCTCTTGGCATCTCTTGGCATCTCTTGGCATCTCTTGGCATCTCTTGG 1686
DB 1091 CAGCTGGATCTCTTGGCATCTCTTGGCATCTCTTGGCATCTCTTGGCATCTCTTGGCATCTCTTGG 1150
QY 1687 AAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1737
DB 1151 ATGACGAGCAGGCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1210
QY 1738 GAGCAGTACACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1797
DB 1211 TGTACCTACGTCAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1270
QY 1798 TCAGCAGTGAATTTATGTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1857
DB 1271 TGATCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1330
QY 1858 TCAAGATGATGATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1917
DB 1331 TCAAGAGAAACGAGTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1390
QY 1918 TGCAGAG 1977
DB 1391 TCAGGAG 1450
QY 1978 ACCTCTCTTTCAGCATGCGACCTGAGG 2004
DB 1451 ATATCATGATCAGATGATTCGCGAAG 1477

RESULT 3

US-08-923-454A-17

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Sequence 17, Application US/08923454A
Patent No. 6004794
GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Livi, George
APPLICANT: Kavian, Eric
APPLICANT: Clinkbeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESS: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2036 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORIGINAL SOURCE: Feature polymorphism at 1325
US-08-923-454A-17

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Query Match      12.8%; Score 384.6; DB 3; Length 2036;
Best Local Similarity 63.7%; Pred. No. 8,6e-83;
Matches 629; Conservative 1; Mismatches 330; Indels 27; Gaps 2;

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QY 1027 CCGCAGGCGAGGTCTCCACGAGTGGAGCGCCGCGTCAAGATTCAACTTCTGCTG 1086
DB 509 CCGGCGGCGCGAGGCGAGGAAGATCCCAAGATTGGCGCATTAATTAATTATCGCGG 568
QY 1087 AGGTGTGAGGAAGATCCGACGCGGTGTGCAACATTAAGCTCTTCCGAGAACACCGCC 1146
DB 569 AGGTGTGAGGAAGATCCGCGCTGCGGTGTGCAATTAATTTGGCAAGCTTCCGT 628
QY 1147 TGTGGCGCGCAGCGTCCCTGTCCAGCGGTTTGGCTTCAATGTGAGAGCGCGCC 1206
DB 629 TTTCTAAAGAGAGGTGGCGGTGGTGAAGTGGTTTATGTGTGGAAGATGAGC 688
QY 1207 TGAATATCAACCAATGCCAGCGTGTGTCCAGCAACAGTGTCTGCGCGCGAGCGACG 1266
DB 689 TGAATGTGAACAATGCCAGCGTGTGTGAACAACA-----GCAACCGGG 730
QY 1267 TCAAGGTGAGCTACAGATGGGAGCTCTATGAGGCCACATCAAGAAGATGACAAAGA 1326

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DB 731 TCAAGGTGAGCTGAGGAAGCGTGTGCACTTACGAAAGCAAAATCAAGATGTGATGAGA 790
QY 1327 AGTGGACATTTGCCACCATCAAGATCATCCCAAGAAAAGCTCCCTGTGTGTGCTGG 1386
DB 791 AAGCAGACATCGCATCTCAAAATTGACACACAGGGCAACTGCTCTCTCGCTGCTTG 850
QY 1387 GTCACTCGGCGGACCTGCGGCGCTGGGAGTTTGTGTGTGCGCATGGGAGTCCCTGGCC 1446
DB 851 GCGGCTCTCTGAGGTGCGGCGGAGAGTTGTGTGTGCGCATGCGAAGCCGTTTCC 910
QY 1447 TACAGAAACAGTGAACAAGGCAATCTGACACTGCGCAGCGGAGGAGGAGGAGCTGG 1506
DB 911 TTCAAAACAGTGAACAAGGAGATCGTGAACAACACCAAGAGGCGGCAAAAGCTGG 970
QY 1507 GCTTCGGGACTCCGACATGACATACATCCAGACGAGATGCCATATCAACTACGGAAC 1566
DB 971 GGTCTCGCACTGACATGACATGACATACATCCAGACCGCATCATCAACTATGGAAC 1030
QY 1567 CCGGGGACCACTGTGTGAACCTGATGAGCGAGTCTATTGGCATCAACAGCTCAAGTCA 1626
DB 1031 CGGAGGCGCGTTAGTAAACCTGACGAGTGAAGTATGAAATTAACCTTTGAAGTGA 1090
QY 1627 CGGCTGCGATCTCTTTGCCATCTCCCTGACACCGCATCAACGAGTTCTCAAGAGTCC 1686
DB 1091 CAGCTGGAATCTCTTTGCCATCTCCATCTGATTAAGATTAAGATTTCTCAAGAGTCC 1150
QY 1687 AAGACAGCAGATCAAG-----ACTGGAAGAGCGCTTCACTGCGCATACGATGC 1737
DB 1151 ATGACCGCAGGCGCAAGAAAGCAAGCATCACCAAGAAAGATATTTGTGTATCCAAATGA 1210
QY 1738 GAGCATATCAACCAAGCCTGTGTGATGAGCTGAAGGCGAGCAACCGGACCTTCCAGAG 1797
DB 1211 TGTCACTACGTCGCAAGAGCGCAAGAGCTGAAGAGACCGGACCGGAGCTTCCAGAG 1270
QY 1798 TCAGCAGTGAATTTATGTGCAAGAGGTTGGCGCCGAATTCACTTCAAGAGGCGGCA 1857
DB 1271 TGATCTCAGAGCGGATTAATTAATGAAGTAAATTCCTGATACCCACAGACAGCTGTG 1330
QY 1858 TCAGAGATGTGACATCATCTGTAAGGTCGAACGCGGCTCTTCTGATGAGCTGAGTAC 1917
DB 1331 TCAAGGAAAGAGCGTCATTAATCAAGCATCAATGACAGTCCGTGTCTCCGCAATGATG 1390
QY 1918 TGCAGAGGCGGTGTGACCGAGTCTCTCTCTCTGATGAGTGTGGGCGGGAAGAGC 1977
DB 1391 TCAAGGAGCTATTAAAGGAAAGACCTTGACATGTGTGTCCGACGAGGATATGAAG 1450
QY 1978 ACCTCTCTTGAAGATCGACCTGAG 2004
DB 1451 ATATCATATCAAGTATTCGGAAG 1477

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RESULT 4
US-08-888-077A-41
Sequence 41, Application US/08888077A

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Patent No. 6020143
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE AND USES THEREFOR.
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESS: LERNER, DAVID, LITENBERG, KRUMHOLZ & MENTLIK
STREET: 600 SOUTH AVENUE WEST
CITY: WESTFIELD
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: ASCII
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/888,077A
/ FILING DATE: 03-JUL-1997
/ CLASSIFICATION: 530
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: US 08/592,541
/ FILING DATE: 26-JAN-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: PALISI, THOMAS M
/ REGISTRATION NUMBER: 36,629
/ REFERENCE/DOCKET NUMBER: SCHERING 3.0-017 CIP CIP IV
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (908) 654-5000
/ TELEFAX: (908) 654-7866
/ INFORMATION FOR SEQ ID NO: 41:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2205 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1..2205
/ OTHER INFORMATION: /note= "multTm1-TM2"
US-08-888-077A-41

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Query Match      12.8%; Score 383.4; DB 3; Length 2205;
Best Local Similarity 63.7%; Pred. No. 1.7e-82;
Matches 629; Conservative 0; Mismatches 331; Indels 27; Gaps 2;

QY 1027 CCGCCAGCGCAGGTCTCCACGAGTGAAGCCCGCGCTCAAGTTCACTTCACTGCTG 1086
DB 585 CTTCCGCGGCGAAGGCGAGGAAGATCCCAAGTTGGCGCCATTAATATACCTTATCGCG 644
QY 1087 ACGGTGTGAGAGATGCGACACCGCTGTCCCATAGAGCTTCTCTGAGACACCGCG 1146
DB 645 ACGTGTGTGAGAGATGCGCCCTCCCGGTTCATATGAGATTTTTCGCAAGCTTCCGT 704
QY 1147 TGTTTGGCGCGAAGGTGCGCTGTCTCAAGCGGTTCGCTTCATATGTCAGAGCGCGCC 1206
DB 705 TTTCTAAACGAGAGGTGCGCGTGTGCTGATGAGGTCTGGGTATATGTGCGAAGATGAC 764
QY 1207 TGATCATCAACCATGCGCAGTGTGTCTCAAGCAAGTGTGCTGCGCGCGAGCAGAC 1266
DB 765 TGATGTGACAAATGCCACGCGGTGACCAACAA-----GACCGCGG 806
QY 1267 TCAAGGTGCACTACAGAAATGGGGAGCTCCTATGAGGCGCACCATCAAGATCGACAGA 1326
DB 807 TCMAAGTTGAGCTGAAGAACGGGTGCTCACTTACGAAGCCAAATCAAGAGATGTGATGAG 866
QY 1327 AGTCGAGATTTGCGACATCAAGATCATCCCAAGAAAAAGTCCCTGTGTGTGCTGG 1386
DB 867 AAGCAGACATGCGACTCATCAAAATTGACACACAGGCGCAAGGTGCTGTCTGCTGTG 926
QY 1387 GTCACTCGGCGCACTCTGGGGGCTTGTGTGGGCGCATCGGCGAGTCCCTTCCGCC 1446
DB 927 GCGCGTCTCTCAAGAGCTGCGCGCGGAGAGATGTGTGTGCGCATCGGAAGCCGCTTTTCC 986
QY 1447 TACAGAACACAGTGAACAGGCGATCTGTGAGCATGCGCCAGCGGAGGAGGAGGAGCTGG 1506
DB 987 TTCMAAACACAGTGAACAGGCGATGTGTGAGCACCCAGCGAGGCGGCAAAAGAGTGG 1046
QY 1507 GCCTCCGGGAGCTTCCGACATGAGTACATCAAGCGAGTCCCATCAATCACTAGGGAAT 1566
DB 1047 GCGTCCGCAACTCAGACATGAGTACATCAAGCGAGCGCATCAATCACTATGGAAT 1106
QY 1567 CCGGAGGAGCACTGTGAGACTGTGAGCGAGGCTCATTTGGCATCAACAGCTCAAGGTCA 1626
DB 1107 CCGGAGGCGCGTTAGTAACTGTGAGCGGTGAATGTGAATTAACCTTTGGAAGTGA 1166
QY 1627 CGGCTGGCATCTCTTGGCATCCCTCAGACCGCATCACAGGTTCTCTACAGAGTTCC 1686

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DB 1167 CAGCTGGAATCTCTTTGCAATCCATCTGATTAAGTTAAAAAGTCCCTCAGGAGTCCC 1226
QY 1687 AAGCAAGCAGATCAAAAG-----ACTGGAAGAGCGCTTCATCGGCATACGGATGC 1737
DB 1227 ATGACGAGCAGGCGCAAGGAAAGAACCATCACCAAGAAAAAGTATTTGGTATCCGAATGA 1286
QY 1738 GAACGATCAACCAAGCTGTGTGATGAGCTGAAGGCGACCAACCGCGACTTCCAGAG 1797
DB 1287 TGTCACTCAGCTCCAGCAAAAGCCAAAGAGCTTGAAGACCGGACCGGAACTTCCAGAG 1346
QY 1798 TCAGCAGTGAATTTATGTCCAAAGAGTTGCGCCGAATTCACCTTCTCAGAGGCGGCA 1857
DB 1347 TGATCTCAGAGAGCGTATATATTAATGAAGTATCTCTGATACCCAGACAGAGCTGTGTC 1406
QY 1858 TCCAAAGTGTGACATCATGTCTCAAGTCAACGGGCGCTCTAGTGAATCTCGAGTACG 1917
DB 1407 TCAAGAAAACGAGGTATATATGACATCAATGAGACGTCCGTGCTCCGCAATGATG 1466
QY 1918 TGCAGAGGCGCGCTGACCGAGTCTCTCTCTCTCTGAGAGTGTGCGGCGGGAACGAG 1977
DB 1467 TCAGGACGTATTTAAAGGAAAGAACCCCTGAACATGTGTGTCCGAGGGTAAATGAG 1526
QY 1978 ACCTCTCTTCAGCATGCGACCTGAGG 2004
DB 1527 ATATCATGATCATCAGTGAATTCGCCAAG 1553

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RESULT 5
US-09-949-016-4643
; Sequence 4643; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4643
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4643

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Query Match      12.7%; Score 383; DB 3; Length 1521;
Best Local Similarity 64.0%; Pred. No. 1.9e-82;
Matches 625; Conservative 0; Mismatches 325; Indels 27; Gaps 2;

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QY 1037 AGGTCTTCCACGAGTGAAGAGCGCGGCTTAAGTTCAATTCATTTGTGAGTGTGA 1096
DB 1 AGGCGAGGAAGATCCCAAGTTGGCGCAATTAATTAATCTTATGCGGAGCTGTGTGA 60
QY 1097 GAAGATGCGACAGCGGTGTGTCACATAGAGTCTTCTGTGAGACACCGCGTGTGGCGG 1156
DB 61 GAGATGCGCGCTGTGCTGTGTTATATGAAATGTTTTCGAAAGCTTCCGTTTCTAAAG 120
QY 1157 CAAGTCCCGCTGTGACGCGTGTGTGCTTCATCATGTGAGAGCGCGGCTGTATCATC 1216
DB 121 AGAGTCCCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
QY 1217 CAATGCCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1276
DB 181 AATGCCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 222

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Oy		127	GCTACAGAAATGGGGACTCCTTATGAGGCCAATCAAAAACAATCGAACAAAGAATGGGCAT	1336
Dd		223	GCTGAGAACGGTGCCACTTTACGAAGCCAAATTCAGAAATGTGATGAAAGCAGACAT	282
Oy		1337	TGCCAACCATCAAATCCATCCCAGAAAAAGCTCCCTGTGTGTGTGTCTGGGTCACTCGGC	1398
Dd		283	CGCACTATCAAAAATTGACACACAGGGGCAAGTGTCTGTCTGTCTGTCTGTGGCGCTCTC	342
Oy		1397	CGAATCGCGGCTTGGGAGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1458
Dd		343	AGAGCTGCGGCGGGAGAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	402
Oy		1457	AGTAGCAACGGGCATTCGTACAGACTGCCACGGGGAGGGGACGGGACGTGGGCTTCGGGA	1516
Dd		403	AGTACCACCGGAGATCTGTAGACACACCAGGAGGCGGCAAAAGGCTGGGGCTTCGGGA	462
Oy		1517	CTCCGACATGGAATACTACATCCAGACGGATGCATCATCACTACGGGAATCCGGGGAGCC	1578
Dd		463	CTCAGACATGGAATCTACATCCAGACGGATGCATCATCACTACGGGAATCCGGGGAGCC	522
Oy		1577	ACTGGTGAACCTGATGGCGAAGTCAATTTGGCATCAACGGCTCAAGTCAAGCTGGCAT	1638
Dd		523	GTTAGTAACCTGACGGTGAAGTGAATTGAATTAACATTGAAAGTGAAGCTGGAT	582
Oy		1637	CTCCTTTGCCATCCCCCTACAGACGGATCAACAGGTTCTCTACAGATTTCCAAGACAGA	1698
Dd		583	CTCCTTTGCCATCCCCCTACAGATTAAGATTAAAGTTCTCTACAGAGTCCCATGACCGCA	642
Oy		1697	GATCAAG-----ACTGGAAGAACGGCTTCACTGGGCATPAGCGATGGCGGACGATCAC	1747
Dd		643	GGCCAAAGAAAAGCCATCACAGAAAGAAATATTTGTATTCGAATGATGTCACTAC	702
Oy		1748	ACCAAGCTGGTGAATGAGCTGAAGAGCCAGAACCCGGACTTCCAGAGGTCAAGATGG	1807
Dd		703	GTCACAGAAACCAAGACGTGAAGAGACCGGACCGGACCTTCCAGACGTGATTCAGG	762
Oy		1808	AATTTATGTGCAAGAGTTGGCGCGAATTAACCTTCTCAAGAGGCGGCATCAAGATGG	1867
Dd		763	AGCGATATTAATTGAAGTAATTCCTGATACCCACAGCAAGCTGGTGTCTCAAGSAAA	822
Oy		1868	TGACATCATGTCACAAGTCAACGGGCGTCTCTGTGTGACTCGATGAGCTGACGAGAGC	1922
Dd		823	CGAGCTCAATTAATGACATCAATGACAGTTCGGTGTCTCCGCAATGATGTACGACGT	882
Oy		1928	CGTGTGACCGAGTCTCTCTCTCTACTGAGAGTGGCGGGGGAACGACGACTTCTT	1987
Dd		883	CATTTAAAGGAAAGCACCTCTGAACATGTGTGTCGCGAGGGGTATGAATATCATAT	942
Oy		1988	CAGCATGCGACCTGAGG 2004	
Dd		943	CACAGTGAATCCCGAAG 959	
 RESULT 6 US-09-724-864-22 ; Sequence 22, Application US/09724864 ; Patent No. 6380362 ; GENERAL INFORMATION: ; APPLICANT: Watson, James D ; APPLICANT: Multison, James G. ; TITLE OF INVENTION: Polynucleotides, polypeptides expressed ; FILE REFERENCE: 11000.1050U ; CURRENT APPLICATION NUMBER: US/09/724,864 ; PRIOR FILING DATE: 2000-11-28 ; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678 ; NUMBER OF SEQ ID NOS: 72 ; SOFTWARE: FastSeq for Windows Version 4.0 ; SEQ ID NO 22 ; LENGTH: 1859 ; TYPE: DNA ; ORGANISM: Mouse				

[illegible]

APPLICANT: Livi, George
APPLICANT: Klinkenbeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1835 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 251...1624
OTHER INFORMATION:
US-08-923-454A-7

Query Match 9.7%; Score 290.6; DB 3; Length 1835;
Best Local Similarity 57.6%; Prid. No. 4e-60;
Matches 577; Conservative 0; Mismatches 394; Indels 30; Gaps 2;

QY 1017 CTGGCCCTTCCGCGCAGGCTCTCCACCAAGTCTAGAGACCCGCGCTACAAGTTCAAC 1076
DB 635 CCGGCGCTCTCGCCGCGCTCTACCGCGCGCGCTTCTCCCGAGTCAAGTCAAC 694
QY 1077 TTCAATTGCTGACGTGTGAGAAAGATCGACACGCGGTGTCAATAGACTCTTCTG 1136
DB 695 TTCATGCGAGATGTGTGAGAAAGACAGACCTCGGTGTATATCGAGATCTGAGAC 754
QY 1137 AGACACCCGCTGTTTGGCGGCAACGTGCCCTGTCCAGGCGTTCGGCTTCACATGCA 1196
DB 755 CGGACCTCTTTCTTGGCGCGGAGTCCCTATCTCGAACGGCTCAAGATTCGTGTGCT 814
QY 1197 GAGGCGGCTGTATCATCAACATGCGCATGTGTCTCAGCAACAGTGTGCGCGGCG 1256
DB 815 GCGGATGGCTATTGTTCACCAACGCCCATGTGTG-----GCTGAT 856
QY 1257 AGGCAAGCTCAAGGTGACCTACAGAAATGGGACTCTATGAGGCCCATCAAAAGAC 1316

DB 857 CCGCGCAGAGTCCGTGTGAGACTGCTAAGCGGCGACAGTATGAGCGCGTGTCAACGT 916
QY 1317 ATCGACAAAGATGGGAGATTGGCCACATCAAGATCATCCCAAGAAAAAGCTCCCTGG 1376
DB 917 GTGATCCCGTGGAGACATGCAACGCGTAGAATTCAGACTTAAGAGAGCTTCCCCACG 976
QY 1377 TTGTTGCTGGGTCACTCGGCGCAGCTCGGCGCTGGGAGATTGTGTGGCCATCGGCACT 1436
DB 977 CTGCTCTGGGACGCTCAGCTGATGTCCGGCAAGGGAGTTTGTGTGCCATGGGAAGT 1036
QY 1437 CCTTGGCCTTACAGAACAGTGAACAAAGGCACTGTCAGACTGCCAGCGGAGAGGC 1496
DB 1037 CCTTTGCACTGCAAGAACAGATCAATCCGCGATTGTAGCTCTGCTCAGGCTCAGGC 1096
QY 1497 AGGAGCTGGGCTCCGGGACTCCGACATGACATTCACAGCGGATGCCATCATCAAC 1556
DB 1097 AAGACCTGGGACTCCCGCAACCAATGTGAATCATTTCAACTGATGACACTTTGAT 1156
QY 1557 TACGGGAATCCGGGGGACCACTGTGTGAACCTGATGGCGAGTCAATTGGCATCAACAG 1616
DB 1157 TTTGAAACTGTGAGGTCCCTGTTAACTGATGGGAGGTGATTTGAGTGAACACAC 1216
QY 1617 CTGAAGTCAAGCTGTGCATCTCTTTGGCATCCCTCAGACCCATCAACGGTTCTTC 1676
DB 1217 ATGAAGTCAAGCTGTGAATCTCTTGGCATCCCTCTGATGCTTCTGAGAGTTTCTG 1276
QY 1677 ACAGAGTCCAAAGACAAAGCA-----GATCAAAAGCTGGAAGAGCGCTTCATC 1724
DB 1277 CATGTGGGAAAGAAAGAAATTCCTCTCCGGAATCAAGGGTCCAGGGGCGCTTACAT 1336
QY 1725 GGCATACGATGTCGAGACATCAACCAAGCTGTGTGATGAGCTGAAGGCCAGCAACCG 1784
DB 1337 GGGGTGATGATGCTGACCTGATCCAGCATCTTGTGAACTACAGCTTGAAGAACCA 1396
QY 1785 GACTTCCCAAGAGTCAAGTGAATTTATGTGCAAGGTTGCCCAATTCACCTTCT 1844
DB 1397 AGCTTTCCGATGTCAAGATGTGTACTCATCTCAATGAATCATCTGGGCTCCCTGCA 1456
QY 1845 CAGAGAGGCGCATCAAGATGTGATCATCTGTCAGATCAAGGTCAGGCGCTCTCTAGTG 1904
DB 1457 CACCGGCTGTCTCTCGGCTGTGTATGTGATTTTGGCCATTGGGGAGCAGATGTACAA 1516
QY 1905 GACTGAGTGAAGCTCAGAGAGCGCGTGTGACCGAGTCTCTCTACTGAGGTTGCGG 1964
DB 1517 AATGCTGAAGATTTTGAAGCTGTTCGAACCCATCCAGTGTGACATGCGATCCGG 1576
QY 1965 CCGGGGAACGACGACTCTCTTCAGCATGCACTTGAGGT 2005
DB 1577 CCGGGACGAGAAACACTGACCTTATATGTGACCCCTGAGGT 1617

RESULT 8
US-09-075-460-4
Sequence 4, Application US/09075460A
Patent No. 6489136
GENERAL INFORMATION:
APPLICANT: Zervos, Antonio S.
TITLE OF INVENTION: CELL PROLIFERATION RELATED GENES
FILE REFERENCE: 10284/004001
CURRENT APPLICATION NUMBER: US/09/075,460A
EARLIER FILING DATE: 1998-05-08
EARLIER APPLICATION NUMBER: US 60/046,077
EARLIER FILING DATE: 1997-05-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (248) ... (1834)
US-09-075-460-4

Query Match 9.7%; Score 290.6; DB 3; Length 2040;
 Best Local Similarity 57.6%; Pred. No. 4.2e-60;
 Matches 577; Conservative 0; Mismatches 394; Indels 30; Gaps 2;

1017 CTGGCCCTTCCCGCAGCGAGCTCTCCACGAGTGAAGCCCGCGTACAGTTCAAC 1076
 |||||
 845 CCGGCGCTCTCGCGCGCTCCAGCCCGCGCGCGCTTCTCCCGAGTGAAGAAC 904
 |||||
 1077 TTCAATGCTGAGTGTGAGAAAGATCGACAGCCGTGTCTACATAGAGCTTTCCG 1136
 |||||
 905 TTCAATGAGATGTGTGAGAAAGACAGACCTGCGTGTCTATATCAGATCTCTGAC 964
 |||||
 1137 AGACACCGCGTGTGTGGCGCAACGTCCTGTCCAGCGGTTCTGGCTTCATATGTA 1196
 |||||
 965 CGGACCCCTTTCTTGGCGCGCGAGTCCCTATCTGAGAGGCTCAGGATCTGTGTGCT 1024
 |||||
 1197 GAGCGCGCTGTATCATCAACATGCCACGTGTGTCCAGCAACAGTCTGCCCGGAC 1256
 |||||
 1025 GCCGATGGGCTCATTTGTACCAACGCCATGTGTG-----GCTGAT 1066
 |||||
 1257 AGGACGACGCTCAAGTGAAGTCAAGAAATGGGACTCTATGAGGCCATCAAGAC 1316
 |||||
 1067 CGGCGCAGAGTCCGTGTGAGACTGTACGCGGCAACGATGAGGCGCTGTGTCAACGT 1126
 |||||
 1317 ATCGACAGAAATGCGGACATTTGCCAATCAAGATCCATCCAGAAAGAGCTCCCTGT 1376
 |||||
 1127 GTGATCCCGTGGCAGACATCGCAACGCTGAGAGATTCAGACTAGAGGCTCTCCACG 1186
 |||||
 1377 TTGTTGCTGGTCACTCGGCGCAGCTGCGCGCTGGGAGTTGTGTGCGCATCGGCACT 1436
 |||||
 1187 CTGCTCTGTGGACGCTCAGCTGATGTCCGGCAAGGGAGTTGTGTGCTCCATGGGAAT 1246
 |||||
 1437 CCCTTGCCCTTACAGAACACAGTGAACAGGGGATGTGTGACGACTGCGCGGAGGCG 1496
 |||||
 1247 CCTTTGCACTGCAAGAACAGATCAATCCGGCATTTGTAGCTGTGCTGAGGCTCAGCGC 1306
 |||||
 1497 AGGGAGTGGGCTCGGGGACTCCGACATGAGCTCATCCAGAGGATCCATCATCAAC 1556
 |||||
 1307 AGAGACTGGGACCTCCCAACCAATGTGAAATTCATTAATCAATGATGACCTATGAT 1366
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 1557 TACGGGAACTCCGGGAGACCACTGTGTGAACCTGTATGGGAGGTCAATGGCATCAACG 1616
 |||||
 1367 TTTGGAATCTGTGAGGTCCCTGTGTAACTGTGATGGGAGGTGATTTGATGAAACAC 1426
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 1617 CTCAAGTCAAGGCTGTGATCTCTTTGCTGATCCCTCAGACCGCATCAACGTTCTTC 1676
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 1427 ATGAAGTCAAGCTGGAATCTCTTTGCTGATCCCTGCTGATGCTTTCGAGAGTTCTG 1486
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 1677 ACAAGATTCAGAGAACGA-----GATCAAGACTGGAAGAAAGGCTTCAATC 1724
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 1487 CATCGTGGGAAAGAAATTCCTCTCCGAAATGATGGGTTCCAGCGGCGCTACAT 1546
 |||||
 1725 GGCATACGATGCGGACGATCAACCAAGCTGTGTGATGAGCTGAAGGCCAGAACCGG 1784
 |||||
 1547 GGGGTGATGATCTGACCTGTAGTCCAGCATCTTTGCTGAATCAAGCTTGAAGAACCA 1606
 |||||
 1785 GACTTCCAGAGCTCAAGAGTGAATTTATGTGCAAGAGTTGCGCGAATTCACCTTCT 1844
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 1607 AGCTTTCCGATGTTTCAAGATGTGTATCATCAATTAAGTATCTCTGGGCTCCCTGCA 1666
 |||||
 1845 CAGAGAGGGGATCCAGATGTGATCATCATGTCAAGTCAACGGGGGTCTCTAAGT 1904
 |||||
 1667 CACCGGCTGTGTCTGGGCTGTGTGATTTTGGCCATTTGGGAGGAGATGTGACAA 1726
 |||||
 1905 GACTGAGTGAAGTGAAGAGCCGTGTGACCGAGTCTCTCTCTCAATGAGGTGCGG 1964
 |||||
 1727 AATGCTGAAGATGTTATTAAGCTGTGTGAACCAATCCAGTTGGCAATGCAAGATCGG 1786
 |||||
 1965 CGGGGAGACGACGACTCTCTTTCAGCATGCACTGAGGT 2005
 |||||
 1787 CGGGGACGAGAAACACTGACTTATATGTGACCCCTGAGGT 1827
 |||||

RESULT 9
 US-08-923-454A-23
 ; Sequence 23, Application US/08923454A
 ; Patent No. 6004794
 ; GENERAL INFORMATION:
 ; APPLICANT: Creasy, Carecha
 ; APPLICANT: Livi, George
 ; APPLICANT: Karian, Eric
 ; APPLICANT: Clinkenbeard, Helen
 ; APPLICANT: Browne, Michael
 ; APPLICANT: Southan, Christopher
 ; TITLE OF INVENTION: HUMAN SERINE PROTEASE
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SmithKline Beecham Corporation
 ; STREET: 709 Swedeland Road
 ; CITY: King of Prussia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19406
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/923,454A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/025436
 ; FILING DATE: 06-SEPT-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Baumeister, Kirk
 ; REGISTRATION NUMBER: 33,833
 ; REFERENCE/DOCKET NUMBER: P50547
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-270-5096
 ; TELEFAX: 610-270-5090
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 23:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2187 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE:
 ; ORIGINAL SOURCE:
 ; FEATURE:
 ; NAME/KEY: Coding Sequence
 ; LOCATION: 603...1976
 ; OTHER INFORMATION:
 ; US-08-923-454A-23

Query Match 9.7%; Score 290.6; DB 3; Length 2187;
 Best Local Similarity 57.6%; Pred. No. 4.3e-60;
 Matches 577; Conservative 0; Mismatches 394; Indels 30; Gaps 2;

1017 CTGGCCCTTCCCGCAGCGAGTCTCCACGAGTGAAGCCCGCGTACAGTTCAAC 1076
 |||||
 987 CCGGCGCTCTCGCGCGCTCCAGCCCGCGCGCGCTTCTCCCGAGTGAAGAAC 1046
 |||||
 1077 TTCAATGCTGAGTGTGAGAAAGATCGACAGCCGTGTCTACATAGAGCTTTCCG 1136
 |||||
 1047 TTCAATGAGATGTGTGAGAAAGACAGACCTGCGTGTCTATATGAGATCTCTGAC 1106
 |||||
 1137 AGACACCGCGTGTGTGGCGCAACGTCCTGTCCAGCGGTTCTGGCTTCATATGTA 1196
 |||||
 1107 CGGACCCCTTTCTTGGCGCGCGAGTCCCTATCTGAAACGCTCAGGATTCGTGTGCT 1166
 |||||

QY 1197 GAGCCGGGCTGATCATCAACAAATGCCAGTGTGTCCAGCAACAGTCTGCCCCGGGC 1256
DB 1167 GCCGATGGGCTCATGTGTACCAACGCCCATGTGTG-----GCTGAT 1208
QY 1257 AGGACAGAGCTCAAGGTGACACTACAGAAATGGGAGTCTATAGAGGCCACCATCAAGAC 1316
DB 1209 CGGCGAGAGTCCGTGTGAGACTGTAAAGGGGAGACGATATAGAGCCGTGTGACAGCT 1268
QY 1317 ATGCACAAAGTTCGACATTTGCCACCATCAAGATTCATCCAAAGAAAAGCTTCCCTGTG 1376
DB 1269 GTGGATCCCGTGGCAGACATCGAACGCTGAGATTCAGCTAAAGAGCTCTCCACAGC 1328
QY 1377 TTGTGTGGGATCACTGGCGGACCTGGCGGCTGGGAGTTGTGGGCGCATCGGACAT 1436
DB 1329 CTGCTCTTGGAGGCTGAGTGTATGTCGGCAAGGGAGTTGTGTGTGCTCATGGAGAT 1388
QY 1437 CCCTTGCCCTTACAGAACACAGTGAACACGAGCATCTGACAGCATGCCCCAGCGGAGAGC 1496
DB 1389 CCCTTGGACCTGACAGAACAGATCAATCGGCAATTTGTAGCTCTGTGACGCGTCCAGCC 1448
QY 1497 AGGAGTGGGCTCTCGGAGCTCGACATGAGACTACATCCAGACGAGTGCATATCAAC 1556
DB 1449 AGGACCTGGGACTCCCGCAACCAATGTGAAATACATTCMACTGATGAGCTATTTGAT 1508
QY 1557 TACGGGAACTCCGGGGGACCACTGTGAACTGTGAACTGTGAGGAGTCAATTGGCATCAACAG 1616
DB 1509 TTTGGAAATCTGTGAGAGTCCCTGTGTAACTGATGAGGAGGTGATTTGATGAGAACACC 1568
QY 1617 CTCAGAGTCACGGCTGGCATCTCTTTGGCCATCCCTCAGACCGCATCAACGAGTTCTTC 1676
DB 1569 ATGAAAGTCAACAGCTGGAATCTCTTTGGCATCCCTTGTGATGCTCTGAGAGTTTCTG 1628
QY 1677 ACAGATTTCCAAACAAAGCA-----GATCAAGACTGGAAGAAAGCGCTTCAATC 1724
DB 1629 CATGTGGGGAAAGAAAGATTTCTCTCCGAAATAGTGGGTCCAGGGCGCTTCATTT 1688
QY 1725 GGCATAGCAGTGGGACGATCAACCAAGCTGTGATGAGCTGAAGGCGACGACCCG 1784
DB 1689 GGGGTATATGTGTGACCTGAGTCCACAGATCTCTGTGAACTACAGCTTGGAGAACCA 1748
QY 1785 GACTTCCCAAGAGTCAAGCTGGAATTTATGTGCAAGAGTGGCGGCAATTCACCTTCT 1844
DB 1749 AGCTTTCGGATTTGACAGATGTGTATCATCATTAAGATCACTCGGCTCTCCCTGCA 1808
QY 1845 CAGAGAGGGGACATCAAGATGTGTACATCATGTCGAAGTCAAGGGGTCTCTAAGT 1904
DB 1809 CACCGGGCTGTGTGCGGCTGTGTATGTATTTGGCCATTTGGGAGACAGATGTACAA 1868
QY 1905 GACTCGAGTGAAGTGCAGAGAGCGGTGTGACCGAGTCTCTCTCACTGAGAGTGGCG 1964
DB 1869 AATGCTGAAGATGTTTATGAGCTGTTCGAACCCATTCAGATTTGGCAATGCAATCCG 1928
QY 1965 CGGGGGAACGACGACTCTCTTTCAGCATGCACTGAGGT 2005
DB 1929 CGGGGACGAGAAACACTGACTTATATGTGACCCCTGAGGT 1969

RESULT 10
US-08-923-454A-24

/ Sequence 24, Application US/08923454A
/ Patent No. 6004794
/ GENERAL INFORMATION:
/ APPLICANT: Creasy, Caretha
/ APPLICANT: Livi, George
/ APPLICANT: Kaitan, Eric
/ APPLICANT: Clinkenbeard, Helen
/ APPLICANT: Browne, Michael
/ APPLICANT: Southan, Christopher
/ TITLE OF INVENTION: HUMAN SERINE PROTEASE
/ NUMBER OF SEQUENCES: 40
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 2187 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 603..1976
OTHER INFORMATION:
US-08-923-454A-24
Query Match 9.7%; Score 290.6; DB 3; Length 2187;
Best Local Similarity 57.6%; Pred. No. 4,3e-60;
Matches 577; Conservative 0; Mismatches 394; Indels 30; Gaps 2;
QY 1017 CTGGCCCTTCCCGCAGGCTCTCCACCAAGCTGAGCAGCCCGGCTTACAGTTCAAC 1076
DB 987 CCGGCGTCTTCGCGCGCGCTTACCGCGCGCGCTTCTCCCGGAGTCACTAACAAC 1046
QY 1077 TTCAATGTGACGTGTGGAAGAAGATGCGACCGCGGTCCACATAGAGCTTCTCTG 1136
DB 1047 TTCAATGAGATGTGTGGAAGAAGACAGACCTGCGGTCTATATGAGATGATCTTGAC 1106
QY 1137 AGACACCCGCTTTTGGCCGCAAGTGCCTGTCCAGCGGTTGTGCTTATCATGTCA 1196
DB 1107 CGGACACCTTTCTTGGGCGGAGAGTCCCTATCTGAAACGCTCAGAAATTTGTGTGCT 1166
QY 1197 GAGCGCGCTGTATCATCAACAAATGCGCAAGTGTGTCAAGAACAGTGTGCCCCGGGC 1256
DB 1167 GCCGATGGGCTCATGTGTACCAACGCCCATGTGTG-----GCTGAT 1208
QY 1257 AGGACAGAGCTCAAGGTGACACTACAGAAATGGGAGTCTATAGAGGCCACCATCAAGAC 1316
DB 1209 CGGCGAGAGTCCGTGTGAGACTGTAAAGGGGAGACGATATAGAGCCGTGTGACAGCT 1268
QY 1317 ATGCACAAAGTTCGACATTTGCCACCATCAAGATTCATCCAAAGAAAAGCTTCCCTGTG 1376
DB 1269 GTGGATCCCGTGGCAGACATCGAACGCTGAGATTCAGCTAAAGAGCTCTCCACAGC 1328
QY 1377 TTGTGTGGGATCACTGGCGGACCTGGCGGCTGGGAGTTGTGGGCGCATCGGACAT 1436
DB 1329 CTGCTCTTGGAGGCTGAGTGTATGTCGGCAAGGGAGTTGTGTGTGCTCATGGAGAT 1388


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QY 1437 CCCTTGCCTTACAGAACACAGTGAACAGGCGATGTGACACTGCTCCAGCGGAGGCG 1496
DB 1389 CTTTTTGCACTGAGAAACAGATCAATCCGGATGTTAGCTCTCTCAGCGCTCACGCC 1448
QY 1497 AGGAGACTGGGCTCCCGGACTCCGACATGACATCAAGACGATGCGATCATCAAC 1556
DB 1449 AAGAGCTTGGACTCCCGCAACCAATGTGAAATACATTCAACTGATGAGTATTGAT 1508
QY 1557 TACGGAACTCCGGGGGACCACTGTGAACTTGTGATGCGAGGTCAATGGCATCAACG 1616
DB 1509 TTTGGAACCTTGAAGTCCCTGTTAACTGTGATGGGAGGTGATTGAGTGAACACC 1568
QY 1617 CTCAAGTCAACGCTGGCATTTCTTTGTCATCTCCCTCAGACCGCATCAACGCTTCTC 1676
DB 1569 ATGAAGTCAACAGTGGAAATCTCTTGTGCACTCCCTGTGATGCTTCTGAGAGTTCTG 1628
QY 1677 ACAGAGTTCAGACAGCAAGCA-----GATCAAGACTGGAAGAGCGCTTCATC 1724
DB 1629 CATCGTGGGAAAGAAAGAAATTCCTCTCCGAAATAGTGGTCCAGCGGCGCTACATT 1688
QY 1725 GGCATACGATGCGAGCATCAACCAAGCTGTGTGATGAGCTGAAGGCCAGCAACCG 1784
DB 1689 GGGGTATGATGCTGACCTGAGTCCAGCATCTTGTGAACTACAGCTTGAAGAACCA 1748
QY 1785 GACTTCCAGAGGTGACAGTGAATTTATGTGCAAGAGGTGCGCGAATTCACCTTCT 1844
DB 1749 AGCTTTCCGATGTTTACAGATGTTTACTCATCAATCAATCTGAGCTCCCTGTGA 1808
QY 1845 CAGAGAGGCGGATCCAGATGTTGATCATCTGCAAGTCAACGGGGGCTCTCTAGT 1904
DB 1809 CACCGGCTGTGCTGCGCGCTGTGATGATTTGGCAATGGGAGGAGATGTACAA 1868
QY 1905 GACTCAGTGAAGTGCAGAGAGCGGTGTGACGAGTCTCTCTCTCAATGAGGTGCG 1964
DB 1869 AATGTGAAGATGTTATGAGTGTTCGAACCAATCCAGTTGCAAGTGCAGATCCGG 1928
QY 1965 CCGGGGACAGACACTCTCTTTGAGCATGCACTGAGGT 2005
DB 1929 CCGGACGAGAAACACTGACTTATATGTGACCCCTGAGGT 1969

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RESULT 11

US-09-008-271A-23
 / Sequence 23, Application US/09008271A
 / Patent No. 6203979
 / GENERAL INFORMATION:

APPLICANT: Bandman, Olga

Bandman, Jennifer L.

Yue, Henry

Guegler, Karl J.

Corley, Neil C.

Tang, Tom Y.

Shah, Purvi

TITLE OF INVENTION: HUMAN PROTEASE MOLECULES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Dr.

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/008,271A

FILING DATE: 16-Jan-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

```

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2476 base pairs
TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SINIDCT01
CLONE: 2680548
SEQUENCE DESCRIPTION: SEQ ID NO: 23 :
US-09-008-271A-23

Query Match      9.7%  Score 290.6; DB 3; Length 2476;
Best Local Similarity 57.6%  Pred. No. 4,5e-60;
Matches 577; Conservative 0; Mismatches 394; Indels 30; Gaps 2;

QY 1017 CTGGCCCTTCCCGCAGGCGAGTCTCCACAGCTGAGACGCCGCGCTACAGTTCAAC 1076
DB 445 CCGGCGTCTCTGCGCGCTGAGCCCGCGCGCGCTTCTTCCCGAGTCAATCAAC 504
QY 1077 TTCAATGCTGACGTGTGAGAGATTCGACACGCGGTGTCACATAGAGCTTCTCTG 1136
DB 505 TTCAATGCTGACGTGTGAGAGATTCGACACGCGGTGTCACATAGAGTCTGAGC 564
QY 1137 AGACACCGGCTGTTGGCGCAACGTCGCTGTCAGCGGTTCTGCTTCAATGTCA 1196
DB 565 CCGCACCTTCTTGGCGCGCGAGGTCTCTATCTGAAACGCTCAGGATTCGTGAGCT 624
QY 1197 GAGCGCGCTGATATCAACCAATGCCAGCGTGTGTCAAGAACAGTGTCCCGGCG 1256
DB 625 GCGATGAGCTCATGTGTACCAACGCCCATGTGTG-----GCTGAT 666
QY 1257 AGGACAGACTCAAGTGCAGCTTACAGATGAGAGGAGCTCTATGAGGCAACATCAAGC 1316
DB 667 CCGCCAGAGTCCGTGTGAGACTGTGATGAGCGGCAAGATGAGGCGGTGTACAGCT 726
QY 1317 ATGCAACAAGTGCAGATTCGCAATTCAGATTCATCCAGAAAAGTCCCTGTG 1376
DB 727 GTGATCCCGTGGCAGACATCGCAACGCTGAGATTCAGACTAAGAGGCTCTCCCAAG 786
QY 1377 TTGTGCTGTGATCATCCGCGCACTGCGGCGCTGTGGGAGTTGTGTGCTCATCGGAGT 1436
DB 787 CTGCTCTGGAGCGCTCAGCTGATGTCCGGCAAGGGAGTTGTGTGCTCATCGGAGT 846
QY 1437 CCCTTGCCTTACAGAACACAGTGAACAGGCGATCTCAGCACTGCCAGCGGAGGCG 1496
DB 847 CCGTTGCACTGAGAAACAGATTCATCCGCGATTTGATGCTGTGCTCAGGCTCAAGC 906
QY 1497 AGGAGCTGGGCTCCGGGACTCCGACATGACATTCATCCAGACGATGCGATCAAC 1556
DB 907 AAGACCTGGGACTCCCGCAACCAATGTGAAATACATTCAAAATGATGAGCTATTGAT 966
QY 1557 TACGGAACTCCGGGGGACCACTGTGAACTGTGATGCGAGGTCAATGGCATCAACG 1616
DB 967 TTTGGAACCTTGAAGTCCCTGTGTAACCTGTGATGCGAGGTGATTTGAGTGAACACC 1026
QY 1617 CTCAAGTCAACGCTGCGATCTCTTTGCAATCCCTCAGACCGCATCAACGCTTCTC 1676
DB 1027 ATGAAGTCAACGCTGAGATCTCTTTGCAATCCCTTGTGATGCTTGTGAGAGTTCTG 1086
QY 1677 ACAGAGTTCAGACAGCA-----GATCAAGACTGGAAGAGGCTTCATC 1724
DB 1087 CATCGTGGGAAAGAAAGAAATTCCTCTCCGAAATCACTGGGTCCACGCGGCTACATT 1146
QY 1725 GGCATACGATGCGAGCATCAACCAAGCTGTGTGATGAGCTGAAGGCCAGCAACCG 1784

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Db 1147 GGGGTATGATGCTGACCTCGATCCGACATCTCTGTAATCAAGCTTCAGAACCA 1206
Qy 1785 GACTTCCAGAGGTGACGACGTGAATTTATGCAAGAGTTGCGCGAATTCACCTTCT 1844
Db 1207 AGCTTCCCATGTTGACGATGTTGTAATCATCATTAAGATTCCTCGGCTCCCTGCA 1266
Qy 1845 CAGAGAGCGGCGATCCAAAGATGTTGACATGATGTCAGGTCAAGGCGCTCTCTAGTG 1904
Db 1267 CACCGGCTGCTGCGGCTGATGATGATTTTGCCATGCGGAGCAGATGTACAA 1326
Qy 1905 GACTCGAGTACGTGACGAGAGCGCTGCTGACCGAGTCTCTCTCACTGAGTGCGG 1964
Db 1327 AATGCTGAAGATTTTATGAAAGCTGTTCAACCCATCCAGTTGGCAGTGCAATCCG 1386
Qy 1965 CGGGGGAACGACGACCTCTCTTTCAGCATGCACTGAGGT 2005
Db 1387 CGGGAGCAGAAACACTGACCTTATATGTGACCCCTGAGGT 1427

RESULT 12

US-09-968-415-23
Sequence 23, Application US/09968415
Patent No. 6855811
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Hillman, Jennifer L.
Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Puri
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,415
FILING DATE: 26-Sep-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/659,151
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SINUCT01
CLONE: 2680548
SEQUENCE DESCRIPTION: SEQ ID NO: 23 :
US-09-968-415-23

Query Match 9.7%; Score 290.6; DB 3; Length 2476;
Best Local Similarity 57.6%; Pred. No. 4.5e-60;

Matches 577; Conservative 0; Mismatches 394; Indels 30; Gaps 2;
Qy 1017 CTGGCCCTTCCCGCAGCGCAGGTCTTCCACCACTGAGACCGCGCTTCAAGTTCAAC 1076
Db 445 CCGGCGGCTCTCCGCGCGCTGCTCCCGCGCGCGCGCTTCTCCCGGAGTCAGTACAA 504
Qy 1077 TTCAATGCGACGTGATGAGAAAGATTCGACCAAGCGGTGTCACATGAGCTTCTCG 1136
Db 505 TTCAATGCGACGTGATGAGAAAGATTCGACCAAGCGGTGTCATATGAGATCTTGAC 564
Qy 1137 AGACACCCGCTGTTGGCGCAACGTGCGCTGTCACAGCGTTCTGCTTCAATGTC 1196
Db 565 CGGCACTCTTCTTGGCGCGAGAGTCCCTATCTGAAACGCTGAGATGTTGCTGCT 624
Qy 1197 GAGGCGGCTGATATATCAACCAATGCCAGCTGTGTCAGACACAGTCTGCGCGGC 1256
Db 625 GCGATGGGCTCATTTGTACCAACGCCCATGTGGT-----GCTGAT 666
Qy 1257 AGGCAAGCTCAAGATGACGTAAGATGGGAGCTCTATGAGGCCACCATCAAGAC 1316
Db 667 CCGCGCAGATCTGTTGAGACTGTAAGCGGCGACGATGAGCGCGGTGACACT 726
Qy 1317 ATCGCAAGAGTCCGACATTTGCCACATCAAGATCCATCCCAAGAAAAGCTCCGTG 1376
Db 727 GTGATCCCGTGGCAGACATCGCAACGCTGAGATTCAGACTTAAGAGACCTTCCACG 786
Qy 1377 TTGTTCTGGGTCACTCGCGCGACCTGCGCTGGGAGTTTGTGTGCTTCCATGGCAGT 1436
Db 787 CTGCTCTGGGACGCTCAGCTGATGTCCGGAAAGGGGATTTGTTGGCCATGGGAGT 846
Qy 1437 CCCTTGCCCTTACAGAACACAGTGAACAGGAGCATTCGACACTGCGCCAGCGGAGGGC 1496
Db 847 CCTTTGACATCGCAAGAACATCAATCAGCTGCGCATTTGACTCTGCTCAGCGTCAACC 906
Qy 1497 AGGAGCTGGGCTTCGCGGACTCCGACATGGAATCAATCCAGACGATGCCATCAAC 1556
Db 907 AGAGACTGGGACCTCCCAACCAATGTGAATTAATTTCAATGATGAGCTGATGAT 966
Qy 1557 TACGGAACTCGGGGGGACACTGTGAACTGTGATGCGAGTCTGATGATCAACG 1616
Db 967 TTTGGAACCTCGAGAGTCCCTGTTAACTGTGAGGGAGGTGATGAGTAAACCC 1026
Qy 1617 CTAAAGTCAAGGCTGCGATCTCTTTCATCTCCATCCCTGACAGCCGATCAACGGTCTC 1676
Db 1027 ATGAAGTCAAGCTGGAATCTCTTTCATCTCCCTTGTGATGCTTTCGAGAGTTTGT 1086
Qy 1677 ACAAGTTCAGACAGCA-----GATCAAGACTGGAGAGCGCTTCATC 1724
Db 1087 CATCGTGGGAAAGAAATTCCTCTCCGGAATCAGTGGGTCCAGCGCGCTACAT 1146
Qy 1725 GGCATACGAGTCCGACGATCAACCAAGCTGTGATGATGATGAGCCAGCAACCG 1784
Db 1147 GGGGTGATGATGACCTTCAATGCCAGATCTCTGTGAACATGACCTTCGAGAACCA 1206
Qy 1785 GACTTCCAGAGTCAAGATGAAATTTATGCAAGAGTTGGCCGAATTCACCTTCT 1844
Db 1207 AGCTTCCCATGTTTACAGATGTGTACTCATTAAGATCATCTCGGCTCCCTGCA 1266
Qy 1845 CAGAGAGCGGCGATCCAAAGATGTGACATCTCTCAAGGTCAACGCGCTCTCTAGTG 1904
Db 1267 CACCGGCTGCTGCGGCTGATGATGATTTTGGCCATTTGGGAGCAGATGTACAA 1326
Qy 1905 GACTCGAGTACGTGACGAGAGCGGTGTCACGAGTCTCTCTCTACTGAGAGTGGG 1964
Db 1327 AATGCTGAAGATTTTATGAAAGCTGTTCAACCCATCCAGTTGGCAGTGCAATCCG 1386
Qy 1965 CGGGGGAACGACGACCTCTCTTCAAGATCGCACTGAGGT 2005
Db 1387 CGGGAGCAGAAACACTGACCTTATATGTGACCCCTGAGGT 1427

RESULT 13

US-08-923-454A-30

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: Sequence 30, Application US/08923454A
: Patent No. 6004794
: GENERAL INFORMATION:
: APPLICANT: Creasy, Caretha
: APPLICANT: Liyi, George
: APPLICANT: Kairan, Eric
: APPLICANT: Clinkebeard, Helen
: APPLICANT: Browne, Michael
: APPLICANT: Southan, Christopher
: TITLE OF INVENTION: HUMAN SERINE PROTEASE
: NUMBER OF SEQUENCES: 40
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SmithKline Beecham Corporation
: STREET: 709 Swedeland Road
: CITY: King of Prussia
: STATE: PA
: COUNTRY: USA
: ZIP: 19406
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ Version 1.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/923,454A
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/025436
: FILING DATE: 06-SEPT-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Baumeister, Kirk
: REGISTRATION NUMBER: 33,833
: REFERENCE/DOCKET NUMBER: P50547
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 610-270-5096
: TELEFAX: 610-270-5090
: TELEX:
: INFORMATION FOR SEQ ID NO: 30:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2187 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: ANTI-SENSE: NO
: HYPOTHEICAL: NO
: ORIGINAL SOURCE:
: FRAGMENT TYPE:
: FEATURE: Polymorphic variants at 672 and 1435
: NAME/KEY: aa24=Arg/Cys aa278=Ala/Val
: LOCATION: 603...1976
: OTHER INFORMATION:
: US-08-923-454A-30

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Query Match 9.6%; Score 289; DB 3; Length 2187;
Best Local Similarity 57.5%; Pred. No. 1e-59;
Matches 576; Conservative 0; Mismatches 395; Indels 30; Gaps 2;

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QY 1017 CTGGCCCTTCCGCGAGGCTGTCACGAGCTGAGAGCCGCGCTTCAAGTTCAAC 1076
DB 987 CCGGCGCTCTCGCGCCGCTCCCTAGCCCGCGCGCTTCTCCCGAGTCAATCAAC 1046
QY 1077 TTCAATGCTGAGCTGTGTGAGAGATCGACAGCCGCTGTCAATAGCTCTTCCG 1136
DB 1047 TTCATCGAGATGTGTGAGAGAGACAGACAGCCGCTGTCTAATATGAGATCTCGAC 1106
QY 1137 AAGACACCCGCTGTGTGAGAGAGCTGCTGTCTGAGGCTTGTGCTTCAATATGTA 1196
DB 1107 CGGACCCCTTCTTGTGGCGCGAGGCTCTATCTCGAAGGCTTGTGTGTGCT 1166
QY 1197 GAGGCCGCGCTATCATCAATGCGCAGTGTGTCTCAGCAACAGTGTGCTGCCCGGCG 1256

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DB 1167 GCCGATGGCTCATTTGTCAACCAAGCCCATGTGGT-----GCTGAT 1208
QY 1257 AGGCAGACCTCTAGAGTCAAGTACAGATGGGAGCTCTTATAGGCCCATCAAGAC 1316
DB 1209 CGGCGCAGAGTCCGTGTGAGCTGTAAAGCGCGCAGAGTATGAGCCGTGTCAACCT 1268
QY 1317 ATCGAAGAAGTGGGAGATTGGCCATCATCAAGATCCATCCCAAGAAAAGCTCCCTGTG 1376
DB 1269 GTGATCCCGTGGAGAGATGCAAGCGGTGAGATTCAGATTAAGAGACCTTCCCAAG 1328
QY 1377 TTGTTGCTGGGTCACTCCGCGAGCTGTGGGCTGTGGGAGTTGTGTGTCATCCGAGT 1436
DB 1329 CTGCTCTGGAGACGTCACTGATGTGTCCGGAGAGGAGTTGTGTGTGTCATGGAGT 1388
QY 1437 CCTTTCGCTTACAGACACAGTGAACAAGGCGATGTCAGACCTGCCAGCGGAGGCG 1496
DB 1389 CCTTTGCACTGAGAACACATCATCCGCGCATTTGTTAGCTCTTCTCAGGCTCAGCC 1448
QY 1497 AGGAGCTGGGCTCCCGGAGCTCCGAGATGACTATCATCAAGAGGATGCCATCATCAAC 1556
DB 1449 AGAGACTGGAGCTCCCGCAACCAATGTGAAATATCAATTCAACTGATGACGCTATTGAT 1508
QY 1557 TACGGAACTCCGGGGAGCACTGGTGAACCTGTGATGCGGAGTCAATGGCATCAACG 1616
DB 1509 TTTGGAACTCTGAGAGTCCCTGTGTAACTGTGATGGGAGTGTATGGATGAACACC 1568
QY 1617 CTCAAGTCAAGCTGTGATCTCTTGTGCAATCCCTTCAAGCCGATCAACGTTCTTC 1676
DB 1569 ATGAAGGTCAAGCTGTGAATCTCTTGTGCAATCCCTTGTGATCTTCTGAGAGTTCTG 1628
QY 1677 ACAGAGTTCGAAGCAACA-----GATCAAGAAGTGGAAAGCGCTCATC 1724
DB 1629 CATGCTGGGAAAGAAAGAAATTTCTCTCCGGAATCAATGGGTCCACAGGCGCTACAT 1688
QY 1725 GGCATACGAGATGCGGACCATCAACAAGCTGTGTGATGAGCTGAAAGCCAGCAACCG 1784
DB 1689 GGGGTGATGATGTGAGTCCCTGATCCAGCATCTGTGTAAGTCAAGCTTCAAGAACCA 1748
QY 1785 GACTTCCAGAGTCAAGTGAAGTTTATGTGCAAGGTTGGCCCAATTCACCTTCT 1844
DB 1749 AGCTTCCGATGTCAAGATGTGTACTCATTCATTAAGTCAATCTGGGCTCCCTGCA 1808
QY 1845 CAGAGAGCGGCTCCAGATGTGATCATCATCGCAAGTCAACGGGCTCTTAGTG 1904
DB 1809 CACCGGCTGTGTGCGGCTGTGTATGTATTTGGCCATTTGGGAGAGATGTATCA 1868
QY 1905 GACTGAGTGAAGTCAAGAGCGGCTGTGAACCGAGTCTCTCTCTACTGAGGTGGCG 1964
DB 1869 AATGCTGAAGATGTTATGAAGCTGTGAAACCAATCCAGTTGGCAGTGAATCCGG 1928
QY 1965 CGGGGAAAGACGACTCTCTTTCAGATCGACCTGAGT 2005
DB 1929 CGGGAGCAGAAACACTGACTTATATGTGACCCCTGAGT 1969

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RESULT 14
US-08-322-742-18
: Sequence 18, Application US/08322742
: Patent No. 5688641
: GENERAL INFORMATION:
: APPLICANT: Sager, Ruth
: TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

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COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: NortonPerfect (Version 5.11)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/322,742
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/938,823
FILING DATE: September 1, 1992
APPLICATION NUMBER: 07/844,236
FILING DATE: February 28, 1992
APPLICATION NUMBER: 07/552,216
FILING DATE: February 28, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00550/048003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 539
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-322-742-18
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Query Match 7.6%; Score 227; DB 2; Length 539;
Best Local Similarity 70.3%; Pred. No. 5.9e-45;
Matches 369; Conservative 0; Mismatches 135; Indels 21; Gaps 4;

QY 1173 AGCGTTTCGGCTTCATCATGAGAGCGCGCTATATCATCAATGCCCGCTGGT 1232
DB 35 AGTGGGTCTGGGTTATGTGTGGAAGATGACTATCGTCAAAATGCCCGCTGGT 94
QY 1233 TCCAGAACAGTGTGCCCCGCGGAGAGAGAGCTCAAGGTGAGTACAGAAATGGGAG 1292
DB 95 ACCAACAA-----GCCACGGGTCAAAAGTTAGCTGAAGAACGGTGC 136
QY 1293 TCCTATAGAGCCCATCAAAAGATGACAAAGATCGGACATTTGCCACCATCAAGATC 1352
DB 137 ACTTAGAAGCCAAATCAAGATGTGATGAGAAAGACAGATCGCATCTCAAAATT 196
QY 1353 CATCCCAAGAAAAGCTCCCTGTGTGTGTCTGTGGTCACTCGGCGACATGGGCTGGG 1412
DB 197 GACCAACAGGCGAAAGCT-GCTGTCTGTGCTGTGGCGCTC-TCAGAGCTGGCGG-CGGGA 253
QY 1413 GAGTTGTGTGGCATTCGCGATGCTCTTCGCTCAAGAACACAGTGAACAAGCGGATC 1472
DB 254 GAGTTGTGTGGCATTCGCGATGCTCTTCGCTCAAGAACACAGTGAACAAGCGGATC 313
QY 1473 GTCAAGACTGCGGAGGAGGAGGAGGAGGAGTGGGCTTCGGGACTTCGACATGACTAC 1532
DB 314 GTGAGACACACCGAGGAGGAGGAGGAGGAGTGGGCTTCGCAACTCAGACATGACTAC 373
QY 1533 ATCCACAGGATGCCATCATCTACAGGAAATCCGGGGAGACCATGTGTGAATCTTGAT 1592
DB 374 ATCCACAGGATGCCATCATCTACAGGAAATCCGGGGAGGCGCGCACTGAACCTGAGC 433
QY 1593 GCGGAGTATTTGGCATCAACAGCTCAAGGTCAAGGCTGCGCATCTCTTTGGCATCCCC 1652
DB 434 GCGGAGTATTTGGCATCAACCTTTGAAGTACAGCTGTGAATCTCTCTCCGCAATCCA 493
QY 1653 TCAGACCGGATCAACAGGTTCTCAGACAGGTTCCAAAGACAAAGCAG 1697
DB 494 TCGATTAAGATTAAAGTTCTCTCAGGAGTCCCATGACCGACAG 538
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RESULT 15
US-08-923-454A-5
; Sequence 5, Application US/08923454A
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Patent No. 6004794
GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Livi, George
APPLICANT: Kairan, Eric
APPLICANT: Clinkenbeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1503 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-923-454A-5
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Query Match 7.2%; Score 217.8; DB 3; Length 1503;
Best Local Similarity 60.8%; Pred. No. 1.4e-42;
Matches 419; Conservative 0; Mismatches 222; Indels 48; Gaps 2;

QY 1017 CTGGCCCTTCCCGGAGGAGTCTCCACAGCTGACAGCCGCGCTACAAATTCAAC 1076
DB 346 CCGGCGTCTTCCGCGCGCTAGCCGCGCGCTTCTCCCGGAGTCAAGTCAAC 405
QY 1077 TTCATTGCTGACGTGTGAAGATCGCACAGCCGCTGTTCACATGAGCTTCTCTG 1136
DB 406 TTCATCGCAGATGTGTGAAGACAGCACTGCGGTCTATATGAGATCCTTGAC 465
QY 1137 AGACACCGCGTGTGGCGGAAAGTGCCCTGTCCAGCGGTTGCTTACATATGCA 1196
DB 466 CCGACCTTCTTGTGGCGGAGGTCTTATCTGAAAGGCTCAGGATGTGTGCT 525
QY 1197 GAGGCGGCTGATCATCAATGCCACAGTGTGTTCAGCAACAGTGTGCTGCCCGGCG 1256
DB 526 GCGGATGGCTCATTTGTACCAAGCCCATGTGGT-----GCTGAT 567
QY 1257 AGGACGACGCTCAAGGTGACGCTACAGATGGGAGCTCTTATGAGGCCACATCAAGAC 1316
DB 568 CCGGCGCAGAGTCCGTGTGAGCTGTAAAGCGGACACAGTATGAGGCGGTGTGACAGCT 627
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QY 1317 ATGCAAGAAAGTCGGAACATTGCCACATCAAGATCCATCCAGAAAAAGCTCCCTGTG 1376
Db 628 GTGGATCCCGTGCGAGACATCCCAAGCTGAGAGATTCAAGCTTAAGAGCCTCTCCCAAG 687
QY 1377 TGTGCTGTGGGTCACTCGGCGGACCTGCGGAGTTGTGTGGCCATCGGAGT 1436
Db 688 CTGCCTGTGGAGCGCTCAAGCTGATGTCCGGCAAGGGAGTTGTGTGGCCATGGGAAT 747
QY 1437 CCTTGCCTTAAGAAACAAGTGACAAAGGCAATGTCAGACATGCCAGCGGAGGAC 1496
Db 748 CCTTGCCTTAAGAAACAAGTGACAAAGGCAATGTCAGACATGCCAGCGGAGGAC 807
QY 1497 AAGGAGCTGGGCTCCGGGACCTCCGACATGACATCAATCCAGACGATGCCATCAAC 1556
Db 808 AAGGAGCTGGGCTCCGGGACCTCCGACATGACATCAATCCAGACGATGCCATCAAC 867
QY 1557 TACGGGAACCTCCGGGAGCACTGTGTAACCT----- 1588
Db 868 TTGGAAACTCTGGAGGTCCCTGTGTAACCTGTGTAAGGAACTGGGGGCTGTATCCCTG 927
QY 1589 --GGATGGGAGGTCAATTGGCATCAACAGCTCAAGGTCAAGGCTGGCATCTCTTTGCC 1646
Db 928 CAGGATGGGAGGTGATTTGAGTGAACACCATGAAGGTCAAGCTGGAATCTCTTTGCC 987
QY 1647 ATCCCTCAGACCGCATCAAGGTTCT 1675
Db 988 ATCCCTTGTGATGTCCTCGAGAGTTCT 1016
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Search completed: February 21, 2006, 18:23:17
Job time : 516 secs

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Qy	1	CAGGAGCTCGAAGTTGACAGTCTCTCA	CACCTCAGTTCCACAGATGTGTAGAGAGG	CAT	60
Db	1	CAGGAGCTCGAAGTTGACAGTCTCTCA	CACCTCAGTTCCACAGATGTGTAGAGAGG	CAT	60
Qy	61	ATTCAGTCCCATTTTTCAGATGAGAGATT	TGAGGCCAGAGAGTAACTTAATCTGTCTGA		120
Db	61	ATTCAGTCCCATTTTTCAGATGAGAGATT	TGAGGCCAGAGAGTAACTTAATCTGTCTGA		120
Qy	121	GGCACACAGAGCTAGAAAGAGCAGAGCC	CAGCCGACCCGATCCCTGTGTGTGTCAGAGCC	CAGC	180
Db	121	GGCACACAGAGCTAGAAAGAGCAGAGCC	CAGCCGACCCGATCCCTGTGTGTGTCAGAGCC	CAGC	180
Qy	181	CCAGTTGCTCATTTGCGGGCTTCGGGAG	CCACGAGCGAGGCTGAGACAGATGTGTTCCAGA		240
Db	181	CCAGTTGCTCATTTGCGGGCTTCGGGAG	CCACGAGCGAGGCTGAGACAGATGTGTTCCAGA		240
Qy	241	TGATGGGAAGCTGAGAGAGACCCGGACA	GAGGCCCGGTGACAGGAAACCCGAGGGCTGTAGGC		300
Db	241	TGATGGGAAGCTGAGAGAGACCCGGACA	GAGGCCCGGTGACAGGAAACCCGAGGGCTGTAGGC		300
Qy	301	CCCGTCACATGATCCTCAGAGCCTGTGTG	TCCTGAGCAGCCCAAGCCCTTACTGTGACG		360
Db	301	CCCGTCACATGATCCTCAGAGCCTGTGTG	TCCTGAGCAGCCCAAGCCCTTACTGTGACG		360

Db	301	CCCGTGCAC	TCGTATGCTC	CAGGCCCTGTGAGTCTTGGACAC	CACAGGCCCTTACGTGCAG	360
Qy	361	GCAGCAGAA	TCAGACCCGGGAA	GGGTCCAGGAAAGTTGTTAA	CCATCTAGCAATGCG	420
Db	361	GCAGCAGAA	TCAGACCCGGGAA	GGGTCCAGGAAAGTTGTTAA	CCATCTAGCAATGCG	420
Qy	421	GGCTGGGGT	GTGTGGCCAA	GTTAAGACACAGATGTAGGG	CCCTGTGGACTCAGAA	480
Db	421	GGCTGGGGT	GTGTGGCCAA	GTTAAGACACAGATGTGTGGCCCTGTGTGA	CTCAGAAATTGGCAG	480
Qy	481	CTCTTTTGG	CCACAGAGGGG	CAAGCTGTGTCCGGGCTTGGGTAG	CTCAGAAAGGTACCT	540
Db	481	CTCTTTTGG	CCACAGAGGGG	CAAGCTGTGTCCGGGCTTGGGTAG	CTCAGAAAGGTACCT	540
Qy	541	GGGGGGCTT	CCACTACACCCCG	CTGGACATCTGCTGTAGCC	CAGGGGCTGGAGGGACC	600
Db	541	GGGGGGCTT	CCACTACACCCCG	CTGGACATCTGCTGTAGCC	CAGGGGCTGGAGGGACC	600
Qy	601	AGCTGAG	AGCCCATGTAGAGAG	GGGCGAGTTCTCTCTGTAA	GGGTATTGCTGTAGATGAG	660
Db	601	AGCTGAG	AGCCCATGTAGAGAG	GGGCGAGTTCTCTCTGTAA	GGGTATTGCTGTAGATGAG	660
Qy	661	GGAA	CAGACAAAGGCC	CCAGGGGACTTAA	CCCGAGATCCAGCCCGGCTCA	720
Db	661	GGAA	CAGACAAAGGCC	CCAGGGGACTTAA	CCCGAGATCCAGCCCGGCTCA	720
Qy	721	GCTC	ACGGCAATATCCTTA	CTCTCTGTAGGCTCTTGCC	CAGCCTTAGAGGGGTCCAGTG	780
Db	721	GCTC	ACGGCAATATCCTTA	CTCTCTGTAGGCTCTTGCC	CAGCCTTAGAGGGGTCCAGTG	780
Qy	781	AGGGGGGTG	AGGAGCC	CAGCAGTGTGAAGCCTTTTAA	CAATTCTCGGGGTGAGCGAC	840
Db	781	AGGGGGGTG	AGGAGCC	CAGCAGTGTGAAGCCTTTTAA	CAATTCTCGGGGTGAGCGAC	840
Qy	841	CCCTTCC	CAATGCTGTGTCTG	CTGCACTGCTGTGTGTGTAGGGGGT	CCCCAACGGGCTC	900
Db	841	CCCTTCC	CAATGCTGTGTCTG	CTGCACTGCTGTGTGTGTAGGGGGT	CCCCAACGGGCTC	900
Qy	901	AGTGTGGG	GTGAGGCTGCTG	CACTGGGACAGGGGGTCTC	AGGAAAGACCTCTCTGCC	960
Db	901	AGTGTGGG	GTGAGGCTGCTG	CACTGGGACAGGGGGTCTC	AGGAAAGACCTCTCTGCC	960
Qy	961	TGCC	CACTGGGCAATAGG	CTTGTGGAGCTGTGAGCATCTGTATCTCA	CTGATGCACTGATGCACTTGG	1020
Db	961	TGCC	CACTGGGCAATAGG	CTTGTGGAGCTGTGAGCATCTGTATCTCA	CTGATGCACTGATGCACTTGG	1020
Qy	1021	CCCTTCC	CGGCGCAGCG	AGGTCTTCACACAGCTGAGCAGCCGGGCT	TCACAAATTCACTTCA	1080
Db	1021	CCCTTCC	CGGCGCAGCG	AGGTCTTCACACAGCTGAGCAGCCGGGCT	TCACAAATTCACTTCA	1080
Qy	1081	TTCGTGA	CGTGTGGAGAA	AGATCGACACAGCGGTGTCC	ACAPAGAGCTTCTCTGAGAC	1140
Db	1081	TTCGTGA	CGTGTGGAGAA	AGATCGACACAGCGGTGTCC	ACAPAGAGCTTCTCTGAGAC	1140
Qy	1141	ACCCGCT	GTTTGGCGGCAAC	GTGCCCTGTCCAGCGGTTCTG	AGCTTCATCATGTCAAGG	1200
Db	1141	ACCCGCT	GTTTGGCGGCAAC	GTGCCCTGTCCAGCGGTTCTG	AGCTTCATCATGTCAAGG	1200
Qy	1201	CCGGCT	GTATCATAC	CAATGCTCCAGTGTGTCC	AGCAAGTGTGCTGCCCGGCGACGGC	1260
Db	1201	CCGGCT	GTATCATAC	CAATGCTCCAGTGTGTCC	AGCAAGTGTGCTGCCCGGCGACGGC	1260
Qy	1261	AGCAGCT	CAAGGTGAC	GTACAGAAATGGGAGCTCT	ATAGGCGCACATCAAAAGACATG	1320
Db	1261	AGCAGCT	CAAGGTGAC	GTACAGAAATGGGAGCTCT	ATAGGCGCACATCAAAAGACATG	1320
Qy	1321	ACA	AAAGTCGACAT	TTCGCAACATCAAGATCC	CAAGAAAAAGCTCCCTGTGTGT	1380
Db	1321	ACA	AAAGTCGACAT	TTCGCAACATCAAGATCC	CAAGAAAAAGCTCCCTGTGTGT	1380
Qy	1381	TGCTGG	GTCACTCGGCG	CACTGCGGCTTGGGAGTTGTGTG	GCATCGGCAGTCCCT	1440

[illegible]

QY 2521 AGGTACATCTGATCCCTTTGGGGGTGGGGGTCCAGCCAGAGCACTGAG 2580
DB 2521 AGGTACATCTGATCCCTTTGGGGGTGGGGGTCCAGCCAGAGCACTGAG 2580
QY 2581 TGAATGCCCCCTGGCTGGAGCTGAGCCCGCTCCATGAGGTTTCTCCCAAGC 2640
DB 2581 TGAATGCCCCCTGGCTGGAGCTGAGCCCGCTCCATGAGGTTTCTCCCAAGC 2640
QY 2641 AGGCAAGAGGCGCGGGAGACGTTGAAAGTTGGCTGCTGGGGAACTTCTCTC 2700
DB 2641 AGGCAAGAGGCGCGGGAGACGTTGAAAGTTGGCTGCTGGGGAACTTCTCTC 2700
QY 2701 CCCAAGGGGCGCATGGGGGAGCTGAGAGGACAGTGAAGTGGAGCTGGGGGTGAG 2760
DB 2701 CCCAAGGGGCGCATGGGGGAGCTGAGAGGACAGTGAAGTGGAGCTGGGGGTGAG 2760
QY 2761 GACTGAGCGGCTTCCCTTCCAGGAGCTCTGGAGTGCAGCAGCGCTCGCATGAG 2820
DB 2761 GACTGAGCGGCTTCCCTTCCAGGAGCTCTGGAGTGCAGCAGCGCTCGCATGAG 2820
QY 2821 TGCCGCCAGAGGCACTGAGGCTGCTGGGCAACCCCTCATCAGGGAAGAGTGT 2880
DB 2821 TGCCGCCAGAGGCACTGAGGCTGCTGGGCAACCCCTCATCAGGGAAGAGTGT 2880
QY 2881 CTCAAGGGGCACTTGGAGCTTGTGTAATGGAATCCAGTGTGCTGTACTGTATG 2940
DB 2881 CTCAAGGGGCACTTGGAGCTTGTGTAATGGAATCCAGTGTGCTGTACTGTATG 2940
QY 2941 TTTCTACTGATGGAATAAAGTTTACAAGCAACGCTTCTAGCCAAATTAATTA 3000
DB 2941 TTTCTACTGATGGAATAAAGTTTACAAGCAACGCTTCTAGCCAAATTAATTA 3000
QY 3001 AAAAAA 3006
DB 3001 AAAAAA 3006

RESULT 2
US-10-617-443B-1
; Sequence 1, Application US/10617443B
; Publication No. US2005001977A1
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew L
; APPLICANT: Qi, Jian-shen
; APPLICANT: Chen, Gailin
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Human PRSS-11 like S2 serine protease and uses thereof
; FILE REFERENCE: ORT-1644
; CURRENT APPLICATION NUMBER: US/10/617,443B
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3006
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-617-443B-1

Query Match 100.0%; Score 3006; DB 8; Length 3006;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3006; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 121 GGCACACAGCTAGAAAGCAAGCCAGCCAGCCGAACCTGTGTGTGACAGCCCCAGC 180
QY 181 CCAAGTTGCTCATTTGGGGGCTCGGAGGCAAGAGGAGCTGAGGAGATGTTCCAGA 240
DB 181 CCAAGTTGCTCATTTGGGGGCTCGGAGGCAAGAGGAGCTGAGGAGATGTTCCAGA 240
QY 241 TGTGTGGAATCTGAGAGAGCCCGGCAAGGCCCTGTGAGGAAACCCGAGGGCTTAGGC 300
DB 241 TGTGTGGAATCTGAGAGAGCCCGGCAAGGCCCTGTGAGGAAACCCGAGGGCTTAGGC 300
QY 301 CCGGTGCCATCTGATCTCTAGGCTGTGTCTGTGACCCAGCCAGCCCTACTGCTAGC 360
DB 301 CCGGTGCCATCTGATCTCTAGGCTGTGTCTGTGACCCAGCCAGCCCTACTGCTAGC 360
QY 361 GCAGAGGAATCTGAGCCCGGGAAGGCTCAAGGGAAGTTGGAACATTAAGCAAGTCG 420
DB 361 GCAGAGGAATCTGAGCCCGGGAAGGCTCAAGGGAAGTTGGAACATTAAGCAAGTCG 420
QY 421 GACTGGGGTGTGGCCCAATTAGACACAGATGAGGGCCCTGTGACTGAGAAATTGGCAG 480
DB 421 GACTGGGGTGTGGCCCAATTAGACACAGATGAGGGCCCTGTGACTGAGAAATTGGCAG 480
QY 481 CTCTTTTGGCCAGAGGGGCAACGCTGTGTCCGGGCTGGGTAGCTCAGAAAGGTCACT 540
DB 481 CTCTTTTGGCCAGAGGGGCAACGCTGTGTCCGGGCTGGGTAGCTCAGAAAGGTCACT 540
QY 541 GGGGGTCTTCCACTACCCCCGCTGTGACACTGTGTAGACCCCAAGGGCTCGAAGGACC 600
DB 541 GGGGGTCTTCCACTACCCCCGCTGTGACACTGTGTAGACCCCAAGGGCTCGAAGGACC 600
QY 601 AGCTGAGGCCCATGAGAGAGGGGCACTTCTCTCTGTAAGGGTATTTCTGTAGAGTAG 660
DB 601 AGCTGAGGCCCATGAGAGAGGGGCACTTCTCTCTGTAAGGGTATTTCTGTAGAGTAG 660
QY 661 GGAACAGACAAAGGCCCAAGGGGCACTAACCCAGATCCAGCCCGGCTCACTCCGTTG 720
DB 661 GGAACAGACAAAGGCCCAAGGGGCACTAACCCAGATCCAGCCCGGCTCACTCCGTTG 720
QY 721 GCTCAGGCAATATCTTAACCTCTCTGTAGAGCTTCTCTCCAGCCCTACAGGGTCAAG 780
DB 721 GCTCAGGCAATATCTTAACCTCTCTGTAGAGCTTCTCTCCAGCCCTACAGGGTCAAG 780
QY 781 AGGGGGGTGAGGAACCCAGACGTAAGAGCTTTTAACATTTCTCGGGGTGACGAGC 840
DB 781 AGGGGGGTGAGGAACCCAGACGTAAGAGCTTTTAACATTTCTCGGGGTGACGAGC 840
QY 841 CCTTCCCAATGCTGTGTGTCTGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
DB 841 CCTTCCCAATGCTGTGTGTGTCTGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 901 AGTGTGGGTGAGGCTGT 960
DB 901 AGTGTGGGTGAGGCTGT 960
QY 961 TGCCCACTGGGATGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
DB 961 TGCCCACTGGGATGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
QY 1021 CCTTCCCGGCAAGCCAGGCTCTCAACAGCTGAGAGCCCGGCTCAACAGTTCAACTTCA 1080
DB 1021 CCTTCCCGGCAAGCCAGGCTCTCAACAGCTGAGAGCCCGGCTCAACAGTTCAACTTCA 1080
QY 1081 TTGCTGAGGTGTGAGAAAGATCGACCAAGCCGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
DB 1081 TTGCTGAGGTGTGAGAAAGATCGACCAAGCCGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
QY 1141 ACCGCTGTTTGGCCGCAAGCGTCCCTGTCAAGGGTTTGGCTTCAATGTGAGAG 1200
DB 1141 ACCGCTGTTTGGCCGCAAGCGTCCCTGTCAAGGGTTTGGCTTCAATGTGAGAG 1200
QY 1201 CCGGCTGATCATCAACCAATGCCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
DB 1201 CCGGCTGATCATCAACCAATGCCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260

QY 1261 AGAGCTCAAGTGGAGCTTATGAGGCCACATCAAGAAATGCG 1320
DB 1261 AGAGCTCAAGTGGAGCTTATGAGGCCACATCAAGAAATGCG 1320
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DB 1321 ACAGAAAGTCGGAATTTGGCCATGATCCCAAGAAAGTCCCTGTGTG 1380
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DB 1381 TGTGGGTCACTGGCCGACCTGGGCTGGGGAGTTTGTGTGCTCGCATG 1440
QY 1441 TGGCCCTAAGAACAGAGTGAACAAGGAGTGTGCACTGCGCCAGCGGAGG 1500
DB 1441 TGGCCCTAAGAACAGAGTGAACAAGGAGTGTGCACTGCGCCAGCGGAGG 1500
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DB 1501 AGCTGGGCTCCGGGACTCCGACATGATCACTCCAGACGATGCACTAG 1560
QY 1561 GGAATCTCGGGGAGCACTGGTGAACCTGGATGGCGAGTCACTGGCATCA 1620
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DB 1621 AGGTCAAGGCTGCTCTCTTGGCCATCCGACGCGATCAAGGATTCGAC 1680
QY 1681 AGTTCAGAACAGAGATCAAGAGTGAAGAGGCTTCACTGGCATACGGA 1740
DB 1681 AGTTCAGAACAGAGATCAAGAGTGAAGAGGCTTCACTGGCATACGGA 1740
QY 1741 CGATCAACCAAGCTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1800
DB 1741 CGATCAACCAAGCTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1800
QY 1801 GCAATCAACCAAGCTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1860
DB 1801 GCAATCAACCAAGCTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1860
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DB 1861 AAGATGTGATCATGCTCAAGAGTCAAGGAGTCTCTAGTGAAGTGAAGTGA 1920
QY 1921 AGGAGGCGGTGCTGACCGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1980
DB 1921 AGGAGGCGGTGCTGACCGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1980
QY 1981 TCCTCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 2040
DB 1981 TCCTCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 2040
QY 2041 GTCAAGCTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 2100
DB 2041 GTCAAGCTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 2100
QY 2101 TGGGCTCTAGAGAGGCGGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2160
DB 2101 TGGGCTCTAGAGAGGCGGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2160
QY 2161 TTGGCCAGGGGCGGAAATTTCCGCTGGGAGTGTGATCAATCCCGTGGG 2220
DB 2161 TTGGCCAGGGGCGGAAATTTCCGCTGGGAGTGTGATCAATCCCGTGGG 2220
QY 2221 GGGAAAGCCCAATCCCTTGTACAGATATCTGAAAGTCACTTCAAGTTCT 2280
DB 2221 GGGAAAGCCCAATCCCTTGTACAGATATCTGAAAGTCACTTCAAGTTCT 2280
QY 2281 ATTCAAAAGTCTTCAAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2340
DB 2281 ATTCAAAAGTCTTCAAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2340

QY 2341 GTGAACACCCATCTGAGATATCCCTGCTCTGCTCTCTCTCTCTCTCTCT 2400
DB 2341 GTGAACACCCATCTGAGATATCCCTGCTCTGCTCTCTCTCTCTCTCTCT 2400
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DB 2401 AAGCTTCTTCCCTCTGACAAACGCGCACTGACCTGAGGCGCCAGCTTCTG 2460
QY 2461 AGGACTTACCAAGCTGTAGGAGCAGAGGCTGCTGCTGCTGCTGCTGCTG 2520
DB 2461 AGGACTTACCAAGCTGTAGGAGCAGAGGCTGCTGCTGCTGCTGCTGCTG 2520
QY 2521 AGGTCAATCTGATCTCTTGGGAGTGGGAGGAGTGGAGTGGAGTGGAGT 2580
DB 2521 AGGTCAATCTGATCTCTTGGGAGTGGGAGGAGTGGAGTGGAGTGGAGT 2580
QY 2581 TGAATGCCCCCTGCTGCGAGCTGAGGCGCCGCTGCACTGAGGTTTCTCT 2640
DB 2581 TGAATGCCCCCTGCTGCGAGCTGAGGCGCCGCTGCACTGAGGTTTCTCT 2640
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DB 2881 CTCAAGGAGGCAATTTGTAGCTTTGCTGTAATGATTTCCAGTGTGCTT 2940
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DB 2941 TTTCTTACTGTATGAAATTAAGTTTCAAGACACAGGTTCTCAGCAAAAA 3000
QY 3001 AAAAAA 3006
DB 3001 AAAAAA 3006

RESULT 3
US-10-485-313A-31
Sequence 31, Application US/10485313A
GENERAL INFORMATION:
APPLICANT: NIE, Guiying
APPLICANT: SALAMONSEN, Lois Adrienne
APPLICANT: LI, Ying
APPLICANT: HAMPTON, Anne Lorraine
APPLICANT: FINDLAY, John Kerr
TITLE OF INVENTION: Novel Serine Protease
FILE REFERENCE: 31633-200357
CURRENT FILING DATE: 2004-01-30
PRIOR APPLICATION NUMBER: PCT/AU02/01010
PRIOR FILING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: PR6707
PRIOR FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
LENGTH: 2543
TYPE: DNA
ORGANISM: Homo sapiens

! TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
! FILE REFERENCE: 031896-043000 (AM 101081)
! CURRENT APPLICATION NUMBER: US/10/956,157
! NUMBER OF SEQ ID NOS: 319805
! SOFTWARE: Patent version 3.2
! SEQ ID NO 5181
! LENGTH: 2541
! TYPE: DNA
! ORGANISM: Homo sapiens
US-10-956-157-5181

Query Match 65.0%; Score 1953; DB 9; Length 2541;
Best Local Similarity 100.0%; Pred. No.0;
Matches 1953; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	589	GGTCTCCACCAAGCTGAGCAGCCCGCGCTACAGTTCAATTGCTGACGTGTGAG	648
QY	1098	AAATGCGACCAAGCCGTGTGCTCAATGAGCTCTTCTGAGACACCCGCTGTTGGCCG	1157
DB	649	AAATGCGACCAAGCCGTGTGCTCAATGAGCTCTTCTGAGACACCCGCTGTTGGCCG	708
QY	1158	AACGTGCCCCCTGTCAGAGCGGTTGCGCTTCATCATGTCAGAGGCGGCGCTGATCATACC	1217
DB	709	AACGTGCCCCCTGTCAGAGCGGTTGCGCTTCATCATGTCAGAGGCGGCGCTGATCATACC	768
QY	1218	AATGCCACGCTGTGTCAGCAACAGTCTGCCCGGAGGAGGAGAGCTCAAGTGTGAG	1277
DB	769	AATGCCACGCTGTGTCAGCAACAGTCTGCCCGGAGGAGGAGAGCTCAAGTGTGAG	828
QY	1278	CTTACAAATGGGGACCTCTATGAGGCCACATCAAAAGCATGCAAAAGTGTGACATT	1337
DB	829	CTTACAAATGGGGACCTCTATGAGGCCACATCAAAAGCATGCAAAAGTGTGACATT	888
QY	1338	GCCACCATCAAGATCCATCCCAAGAAAAGCTCCCTGTGTTGCTGGGGTCACTGGGC	1397
DB	889	GCCACCATCAAGATCCATCCCAAGAAAAGCTCCCTGTGTTGCTGGGGTCACTGGGC	948
QY	1398	GACCTGCGGCTGGGGAGTTTGTGTGGCCATGGGAGTCCCTTCGCTTACAGAACACA	1457
DB	949	GACCTGCGGCTGGGGAGTTTGTGTGGCCATGGGAGTCCCTTCGCTTACAGAACACA	1008
QY	1458	GTGACAAAGGGGACCTCTGAGCACTGCCACGCGGAGGAGGAGGAGCTGGGGCTCCGGGAC	1517
DB	1009	GTGACAAAGGGGACCTCTGAGCACTGCCACGCGGAGGAGGAGGAGGAGCTGGGGCTCCGGGAC	1068
QY	1518	TCCGACATGGAATCATCCAGACGATGTCATCATCACTACGGGAATCCCGGGGAGCA	1577
DB	1069	TCCGACATGGAATCATCCAGACGATGTCATCATCACTACGGGAATCCCGGGGAGCA	1128
QY	1578	CTGGTGAACCTGTGATGGCAGAGTTCATTTGGCATCAACGCTCAAGGTCAAGCTGTGCATC	1637
DB	1129	CTGGTGAACCTGTGATGGCAGAGTTCATTTGGCATCAACGCTCAAGGTCAAGCTGTGCATC	1188
QY	1638	TCTTTGGCATCCCTTCAGACCGGCATCAACGCTTCTTCAAGAGTTTCAAGACAGCAG	1697
DB	1189	TCTTTGGCATCCCTTCAGACCGGCATCAACGCTTCTTCAAGAGTTTCAAGACAGCAG	1248
QY	1698	ATCAAGAAGCTGAAGAGCGCTTCATGCGCATGCGATGCGAGCATCAACCAAGCTG	1757
DB	1249	ATCAAGAAGCTGAAGAGCGCTTCATGCGCATGCGATGCGAGCATCAACCAAGCTG	1308
QY	1758	GTGGATGAGCTGAAGGCGCAACCCGGAATTCCAGAGGTCAAGAGTGAATTATGTG	1817
DB	1309	GTGGATGAGCTGAAGGCGCAACCCGGAATTCCAGAGGTCAAGAGTGAATTATGTG	1368
QY	1818	CAAGAGGTGGCGCGGAATTCATCTTCAAGAGGCGGATCCAAAGTGTGACATCATC	1877
DB	1369	CAAGAGGTGGCGCGGAATTCATCTTCAAGAGGCGGATCCAAAGTGTGACATCATC	1428

QY	1878	GTCAAGGTCAACGGGCGTCTCTAGTGACTGAGTGAAGCTGCAGAGGCGGTGACCC	1937
DB	1429	GTCAAGGTCAACGGGCGTCTCTAGTGACTGAGTGAAGCTGCAGAGGCGGTGACCC	1488
QY	1938	GAGTCTCTCTCTACTGAGGTGCGCGGGGAAAGAGACCTTCCTTCAGATCGCA	1997
DB	1489	GAGTCTCTCTCTACTGAGGTGCGCGGGGAAAGAGACCTTCCTTCAGATCGCA	1548
QY	1998	CCTGAGGTGTATGTGAGGGGCGCATTCCTTCAGCGCCCAAGCTTCAGAGCTGCAGACA	2057
DB	1549	CCTGAGGTGTATGTGAGGGGCGCATTCCTTCAGCGCCCAAGCTTCAGAGCTGCAGACA	1608
QY	2058	ACGAGGGGAGCGCCCCCGGATCAGAGCAAGAGCAACCGTGTCTTCAGAGGAGC	2117
DB	1609	ACGAGGGGAGCGCCCCCGGATCAGAGCAAGAGCAACCGTGTCTTCAGAGGAGC	1668
QY	2118	GGCAGCTTCCTCTGTGCTGTCCGAGGAGAGCGAGGCTGGCTTGGCCAGGGGCGGAA	2177
DB	1669	GGCAGCTTCCTCTGTGCTGTCCGAGGAGAGCGAGGCTGGCTTGGCCAGGGGCGGAA	1728
QY	2178	TTTCCGCGCTGGGGAATGTTGATCCACATCCCGGTGCGGGGAGGGAAGCCCAATGCC	2237
DB	1729	TTTCCGCGCTGGGGAATGTTGATCCACATCCCGGTGCGGGGAGGGAAGCCCAATGCC	1788
QY	2238	CTTGTACAGATGATCTGAAAGTCACTTCAAGTTCTCCGGAATTCACAAATGCTCTT	2297
DB	1789	CTTGTACAGATGATCTGAAAGTCACTTCAAGTTCTCCGGAATTCACAAATGCTCTT	1848
QY	2298	CCATGAGAGTCCCTCTCTCTAGCTTCCGCTCTGCGCTGTGAAACCCCATCTGCA	2357
DB	1849	CCATGAGAGTCCCTCTCTCTAGCTTCCGCTCTGCGCTGTGAAACCCCATCTGCA	1908
QY	2358	GTATCCCTGCTCCCGCCCT	2417
DB	1909	GTATCCCTGCTCCCGCCCT	1968
QY	2418	ACAAAGCGCCACCTGACCTGAGGCGCCGACCTTCCCTCTGCTTACCAAGCTGT	2477
DB	1969	ACAAAGCGCCACCTGACCTGAGGCGCCGACCTTCCCTCTGCTTACCAAGCTGT	2028
QY	2478	AGGCGCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2537
DB	2029	AGGCGCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2088
QY	2538	TTTGGGGGTGGGGGTGGGGGTGGGGGTGGGGGTGGGGGTGGGGGTGGGGGTGGGGGTGG	2597
DB	2089	TTTGGGGGTGGGGGTGGGGGTGGGGGTGGGGGTGGGGGTGGGGGTGGGGGTGGGGGTGG	2148
QY	2598	CGAGCTGAGCCCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2657
DB	2149	CGAGCTGAGCCCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2208
QY	2658	GAGCAGTGAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2717
DB	2209	GAGCAGTGAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2268
QY	2718	GCAAGCTGCAAGAGCAATGAGACGTGAGCTGCGGGGTGTAAGAGCTGAGGCGGCTTCC	2777
DB	2269	GCAAGCTGCAAGAGCAATGAGACGTGAGCTGCGGGGTGTAAGAGCTGAGGCGGCTTCC	2328
QY	2778	CTTCCACGACGCTCTGGGATGACAGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2837
DB	2329	CTTCCACGACGCTCTGGGATGACAGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2388
QY	2838	CAGGCTGCTGGGACCAACCCCTCTCATCAAGGGAACGAGTGTGTCTCAAGGGGCAATTTGTG	2897
DB	2389	CAGGCTGCTGGGACCAACCCCTCTCATCAAGGGAACGAGTGTGTCTCAAGGGGCAATTTGTG	2448
QY	2898	AGCTTGTGTAAATGATTCCTCAGTGTGTCTTGTACGTATGTTTCTCTACTGATGGA	2957
DB	2449	AGCTTGTGTAAATGATTCCTCAGTGTGTCTTGTACGTATGTTTCTCTACTGATGGA	2508
QY	2958	AAATTAAGTTTACAGACACGCTTCTGAGCA 2990	

Db 2509 AATTAAGTTTACAAAGCACACCGTTCTCAGCCA 2541

RESULT 5
US-09-818-143-14
Sequence 14, Application US/09818143
Patent No. US20020019000A1
GENERAL INFORMATION:
APPLICANT: Walker, Michael G.
APPLICANT: Volkmuth, Wayne
APPLICANT: Klingler, Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES COEXPRESSED WITH MATRIX-REMODELING GENES
FILE REFERENCE: PB-0004 CIP
CURRENT APPLICATION NUMBER: US/09/818,143
NUMBER OF FILING DATE: 2001-03-26
SOFTWARE: PERL Program
SEO ID NO 14
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: -
OTHER INFORMATION: 2814981CB1
US-09-818-143-14

Query Match 64.9%; Score 1949.4; DB 3; Length 2040;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1956; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1038 GGTCTCCACCAAGCTAGAGACCCCGGCTCAAGTTCAACTTGTCTGAGCGTGGAG 1097
DB 72 GGTCTCCACCAAGCTAGAGACCCCGGCTCAAGTTCAACTTGTCTGAGCGTGGAG 131
QY 1098 AAGATCGACACACCGGTGTCCACATAGAGCTTCTCTGAGACACCCGCTGTTGGCCGC 1157
DB 112 AAGATCGACACACCGGTGTCCACATAGAGCTTCTCTGAGACACCCGCTGTTGGCCGC 191
QY 1158 AAGGTGCTGTCTGAGCGGTGTCTGCTTCAATGTCAGAGCGCGCTGATCATCACC 1217
DB 192 AAGGTGCTGTCTGAGCGGTGTCTGCTTCAATGTCAGAGCGCGCTGATCATCACC 251
QY 1218 AATGCCACGTGTGTCCAGCAAGTGTGCGCGCGGACAGGACGCTCAAGGTGAG 1277
DB 252 AATGCCACGTGTGTGTCCAGCAAGTGTGCGCGCGGACAGGACGCTCAAGGTGAG 311
QY 1278 CTACAGAAATGGGGAATCTCTATGAGGACCAATCAAGAATCGACAGAAATCGGACAT 1337
DB 312 CTACAGAAATGGGGAATCTCTATGAGGACCAATCAAGAATCGACAGAAATCGGACAT 371
QY 1338 GGCACATCAAGATCATCCCAAGAAAAGCTCCCTGTGTGTGTGCTGGGTCACTCGGC 1397
DB 372 GGCACATCAAGATCATCCCAAGAAAAGCTCCCTGTGTGTGTGCTGGGTCACTCGGC 431
QY 1398 GACCTGCGGCTGGGGAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1457
DB 432 GACCTGCGGCTGGGGAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 491
QY 1458 GTGACAAAGGATGT 1517
DB 492 GTGACAAAGGATGT 551
QY 1518 TCCGACATGATCAATCAAGACGATGTCATCACTAATCGGAACTCCGGGGAGCA 1577
DB 552 TCCGACATGATCAATCAAGACGATGTCATCACTAATCGGAACTCCGGGGAGCA 611
QY 1578 CTGGGGAATCTGGGGAATCTGGGGAATCTGGGGAATCTGGGGAATCTGGGGAATCT 1637
DB 612 CTGGGGAATCTGGGGAATCTGGGGAATCTGGGGAATCTGGGGAATCTGGGGAATCT 671
QY 1638 TCTCTTGGCATCTCTGAGACCGCATCAACCGTTCTCTGACAGAGTTCCAAAGCAAG 1697
DB 672 TCTCTTGGCATCTCTGAGACCGCATCAACCGTTCTCTGACAGAGTTCCAAAGCAAG 731

QY 1698 ATCAAAGATGGAAGAGCGCTTCAATGCGGATGCGGAGCATCAACCAAGCCG 1757
DB 732 ATCAAAGATGGAAGAGCGCTTCAATGCGGATGCGGAGCATCAACCAAGCCG 791
QY 1758 GTGATGATGATGAAGGACGAGAACCCGGAATCTCCAGAGGTGAGAGTGAATTTATGTG 1817
DB 792 GTGATGATGATGAAGGACGAGAACCCGGAATCTCCAGAGGTGAGAGTGAATTTATGTG 851
QY 1818 CAAGAGTTGGCGGGAATTCATCTTCTGAGAGAGGCGCATCAAGATGTGATCATC 1877
DB 852 CAAGAGTTGGCGGGAATTCATCTTCTGAGAGAGGCGCATCAAGATGTGATCATC 911
QY 1878 GTCAAGGTCAACGCGGCTCTCTAGTGAATCTGATGAGCTGACAGAGGCGGTGTCACC 1937
DB 912 GTCAAGGTCAACGCGGCTCTCTAGTGAATCTGATGAGCTGACAGAGGCGGTGTCACC 971
QY 1938 GAGTCT 1997
DB 972 GAGTCT 1031
QY 1998 CTTGAGGTGTCTATGAGGAGGCGCATTTCTTCAAGCGCAAGCTCTCAAGCTGACACA 2057
DB 1032 CTTGAGGTGTCTATGAGGAGGCGCATTTCTTCAAGCGCAAGCTCTCTCAAGCTGACACA 1091
QY 2058 ACGAGGAGGACG 2117
DB 1092 ACGAGGAGGACG 1151
QY 2118 GGCAGCT 2177
DB 1152 GGCAGCT 1211
QY 2178 TTTCCGCTGGGAGTGTGATTCATCCCGGTGCGGAGGAAACCAATCCC 2237
DB 1212 TTTCCGCTGGGAGTGTGATTCATCCCGGTGCGGAGGAAACCAATCCC 1271
QY 2238 CTGTGACAGATGATCTGAAAGTCACTTCCAAAGTCTCCGATATTCAAAGCGCTT 2297
DB 1272 CTGTGACAGATGATCTGAAAGTCACTTCCAAAGTCTCCGATATTCAAAGCGCTT 1331
QY 2298 CCATGAGAGTCCCT 2357
DB 1332 CCATGAGAGTCCCT 1391
QY 2358 GTATCCCTGCT 2417
DB 1392 GTATCCCTGCT 1451
QY 2418 ACAAAAGCCCACTGACCTGAGGCGCCAGCTTCTCTGCTGTAGACTTACCAAGCTGT 2477
DB 1452 ACAAAAGCCCACTGACCTGAGGCGCCAGCTTCTCTGCTGTAGACTTACCAAGCTGT 1511
QY 2478 AGGAGCAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2537
DB 1512 AGGAGCAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1571
QY 2538 TTTGGGAGTGGGAGTGGGAGTCCAGCCAGACAGGACCTGAGTGAATGCCCTGAGCTG 2597
DB 1572 TTTGGGAGTGGGAGTGGGAGTCCAGCCAGACAGGACCTGAGTGAATGCCCTGAGCTG 1631
QY 2598 CGGAGCTGAGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2657
DB 1632 CGGAGCTGAGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1691
QY 2658 GAGCAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2717
DB 1692 GAGCAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1751
QY 2718 GCAAGCTGCAAGGACATGAGCTGAGCTGCGGAGTGTGAGGACCTGAGCCGAGCTTCCC 2777
DB 1752 GCAAGCTGCAAGGACATGAGCTGAGCTGCGGAGTGTGAGGACCTGAGCCGAGCTTCCC 1811

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OY 2778 TTCCACGACGACCTTGGGATGACGACAGCCGCTGCATGGAAGTGCCTCCAGAGCATG 2837
DB 1812 CTTCACGACGACCTTGGGATGACGACAGCCGCTGCATGGAAGTGCCTCCAGAGCATG 1871
OY 2838 CAGCGTCGTGGGACCAACACCCCTCTCATCCAGGGAAAGATGTGTCTCAAGGGGCAATTGTG 2897
DB 1872 CAGCGTCGTGGGACCAACACCCCTCTCATCCAGGGAAAGATGTGTCTCAAGGGGCAATTGTG 1931
OY 2898 AGCTTGTCTGTAATGAAATTCACGATGTGCTTGTACTGTAATGTTTCTTACTGTATGGA 2957
DB 1932 AGCTTGTCTGTAATGAAATTCACGATGTGCTTGTACTGTAATGTTTCTTACTGTATGGA 1991
OY 2958 AATTAAGTTTACAGACACAGCGTCTCAGCCAAAAA 3004
DB 1992 AATTAAGTTTACAGACACAAAAA 2038

RESULT 6
US-09-796-753-31
; Sequence 31, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29

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; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 31
;
; LENGTH: 2576
;
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-753-31

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Query Match	54.6%	Score 1942.8	DB 3	Length 2576
Best Local Similarity	99.4%	Pos. No. 0		
Matches 1950	Conservative	Pred. Matches	12	Indels 0
		Gaps	0	
QY	1038	GGTCTCCACCAAGCTGAGACAGCCCGCGCTCAACAAGTTCAACTTCATTCGTCAGCGTGGTAG	1097	
DB	606	GGTCTCCACCAAGCTGAGACAGCCCGCGCTCAACAAGTTCAACTTCATTCGTCAGCGTGGTAG	665	
QY	1098	AAGATCGCACAGCCCGTGTCTCAATATGAGCTCTTCTTGAGACACCCGCTGTTGGCCGC	1157	
DB	666	AAGATCGCACAGCCCGTGTCTCAATATGAGCTCTTCTTGAGACACCCGCTGTTGGCCGC	725	
QY	1158	AACGTGCCCTGTCTCCAGGCGTTTCTGGCTTCATCATGTCAAGAGGCGCGCTGATCATACC	1217	
DB	726	AACGTGCCCTGTCTCCAGGCGTTTCTGGCTTCATCATGTCAAGAGGCGCGCTGATCATACC	785	
QY	1218	AATGCCCACTGTGTCTCAGCAACAGTGTCTCCCGGCGCAGCGACAGCTTCAAGTGTACG	1277	
DB	786	AATGCCCACTGTGTCTCAGCAACAGTGTCTCCCGGCGCAGCGACAGCTTCAAGTGTACG	845	
QY	1278	CTACAGAAATGGGGACCTCCTATAGAGGCCACCATCAAAACATTCGACAAAGTGGGACATT	1337	
DB	846	CTACAGAAATGGGGACCTCCTATAGAGGCCACCATCAAAACATTCGACAAAGTGGGACATT	905	
QY	1338	GCCACCATCAAGATTCATCCCAAGAAAAAGCTCCCTGTGTGTTGTTCTGGGTCACTCGGCC	1397	
DB	906	GCCACCATCAAGATTCATCCCAAGAAAAAGCTCCCTGTGTGTTGTTCTGGGTCACTCGGCC	965	
QY	1398	GACCTGGGGCTGGGGAGTTTGTGTGGCCATGGGACAGTCCCTTGGCCCTACAGAACACA	1457	
DB	966	GACCTGGGGCTGGGGAGTTTGTGTGGCCATGGGACAGTCCCTTGGCCCTACAGAACACA	1025	
QY	1458	GTGACCAACGGGCACTCTGTACACACTGCCACAGGAGGGGAGGAGCTGTGGCTCCGGAC	1517	
DB	1026	GTGACCAACGGGCACTCTGTACACACTGCCACAGGAGGGGAGGAGCTGTGGCTCCGGAC	1085	
QY	1518	TCCGACATGCACTACATCCACAGCGGATGCCATCACTACCGGAACTCCGGGGAGCCA	1577	
DB	1086	TCCGACATGCACTACATCCACAGCGGATGCCATCACTACCGGAACTCCGGGGAGCCA	1145	
QY	1578	CTGGTGAAACCTGGATGCGAGGATCATTTGGGATCAACACGCTCAAGGTCACGGCTGGGATC	1637	
DB	1146	CTGGTGAAACCTGGATGCGAGGATCATTTGGGATCAACACGCTCAAGGTCACGGCTGGGATC	1205	
QY	1638	TCTCTTTCGCATCCCTCTCAGACCGGATCACACGGTCTCTCAAGAGTTCAAAGACAGCAG	1697	
DB	1206	TCTCTTTCGCATCCCTCTCAGACCGGATCACACGGTCTCTCAAGAGTTCAAAGACAGCAG	1265	
QY	1698	ATCAAAACCTGGAAAGAGCGCTTCATTCGGATACGGATGGGAGAGTCAACCAAGGCTG	1757	
DB	1266	ATCAAAACCTGGAAAGAGCGCTTCATTCGGATACGGATGGGAGAGTCAACCAAGGCTG	1325	
QY	1758	GTGATGAGCTGAAAGGCGACCAACCCGCACTTCCAGAGGTCACAGTGAATTTATGTG	1817	
DB	1326	GTGATGAGCTGAAAGGCGACCAACCCGCACTTCCAGAGGTCACAGTGAATTTATGTG	1385	
QY	1818	CAAGAGGTTGCGCGGAATTAACCTTCTCAGAGAGGCGGACATCCAAGTGGTGACATATC	1877	
DB	1386	CAAGAGGTTGCGCGGAATTAACCTTCTCAGAGAGGCGGACATCCAAGTGGTGACATATC	1445	

QY 1878 GTCAAGGTCAACGCGGCTCTCTAGTGAAGCTGAGGAGCGGCTGACC 1937
DB 1446 GTCAAGGTCAACGCGGCTCTCTAGTGAAGCTGAGGAGCGGCTGACC 1505
QY 1938 GAGTCTCTCTCTCTAGTGAAGTGCAGCGGAGAAAGAGACCTCTCTTCAAGATCGCA 1997
DB 1506 GAGTCTCTCTCTCTAGTGAAGTGCAGCGGAGAAAGAGACCTCTCTTCAAGATCGCA 1565
QY 1998 CTTGAGGTGTATGTAGAGGCGCATTTCTTCAAGCGCAAGCTGCAAGCTCGAGACA 2057
DB 1566 CTTGAGGTGTATGTAGAGGCGCATTTCTTCAAGCGCAAGCTGCAAGCTCGAGACA 1625
QY 2058 ACGAGGAGGAGCGCGCGCGCGAGATCAGAGCAACGCGGTCTTCAAGAGAGG 2117
DB 1636 ACGAGGAGGAGCGCGCGCGCGAGATCAGAGCAACGCGGTCTTCAAGAGAGG 1685
QY 2118 GGCAGCTCTCTCTCTGAGTGTCCGAGGAGAGAGGCTTGGCCAGGAGGCGCGCA 2177
DB 1686 AGCAGCTCTCTCTCTGAGTGTCCGAGGAGAGAGGCTTGGCCAGGAGGCGCGCA 1745
QY 2178 TTTCCGCTGAGGAGTGTGATTCACATCCGAGTGCAGGAGAGGAGCCCAATCCC 2237
DB 1746 TTTCCGCTGAGGAGTGTGATTCACATCCGAGTGCAGGAGAGGAGCCCAATCCC 1805
QY 2238 CTTGTAAGATGATCTGAAAGTCACTTCAAGTTCTCCGATTTCAAAATGCGCTT 2297
DB 1806 CTTGTAAGATGATCTGAAAGTCACTTCAAGTTCTCCGATTTCAAAATGCGCTT 1865
QY 2298 CCATGAGGATCCCTCTCTCTCTAGCTTCCGCTTGCCTGTAAGACCATCTGCA 2357
DB 1866 CCATGAGGATCCCTCTCTCTCTAGCTTCCGCTTGCCTGTAAGACCATCTGCA 1925
QY 2358 GTATCCCTGCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2417
DB 1926 GTATCCCTGCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1985
QY 2418 ACAAAAGCCCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2477
DB 1986 ACAAAAGCCCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2045
QY 2478 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2537
DB 2046 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2105
QY 2538 TTTGGGAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2597
DB 2106 TTTGGGAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2165
QY 2598 CGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2657
DB 2166 CGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2225
QY 2658 GAGCAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2717
DB 2226 GAGCAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2285
QY 2718 GAGCAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2777
DB 2286 GAGCAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2345
QY 2778 CTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2837
DB 2346 CTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2405
QY 2838 CAGGCTGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2897
DB 2406 CAGGCTGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2465
QY 2898 AGCTTTGCTGTAAGATGATTCAGAGTGTGCTGTAAGTGTGCTGTAAGTGTGCTGTAAGTGA 2957
DB 2466 AGCTTTGCTGTAAGATGATTCAGAGTGTGCTGTAAGTGTGCTGTAAGTGTGCTGTAAGTGA 2525
QY 2958 AATTAAGTTTCAAGCAGCAGGTTCTCAGCAAAAAA 2999

DB 2526 AATTAAGTTTCAAGCAGCAGGTTCTCAGCAAAAAA 2567
RESULT 7
US-09-764-898-112
; Sequence 112, Application US/09764898
; Patent No. US7002090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1201
; CURRENT APPLICATION NUMBER: US/09/764,898
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 112
; LENGTH: 1868
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-898-112
Query Match 60.3%; Score 1813.8; DB 3; Length 1868;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1818; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
QY 1174 GCGGTTCTGCTTCAATGTCAGAGGCGGCTGATCATCAATGCCAGTGTGT 1233
DB 21 GCGGTTCTGCTTCAATGTCAGAGGCGGCTGATCATCAATGCCAGTGTGT 80
QY 1234 CCAAGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1293
DB 81 CCAAGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 140
QY 1294 CTTATGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1353
DB 141 CTTATGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 200
QY 1354 ATCCCAAGAAAAAGTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1413
DB 201 ATCCCAAGAAAAAGTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 260
QY 1414 AGTTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1473
DB 261 AGTTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 320
QY 1474 TCAGCAGTCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1533
DB 321 TCAGCAGTCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 380
QY 1534 TCAGCAGTCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1593
DB 381 TCAGCAGTCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 440
QY 1594 GCGAGTCAATTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1653
DB 441 GCGAGTCAATTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 500
QY 1654 CAGACCGATCAACAGGTTCTCAGAGGTTCCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAG 1713
DB 501 CAGACCGATCAACAGGTTCTCAGAGGTTCCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAG 560
QY 1714 AGCGCTTATCGGATCAAGATGCGAGATCAACCAAGCTGTGTGATGAGTGAAGG 1773
DB 561 AGCGCTTATCGGATCAAGATGCGAGATCAACCAAGCTGTGTGATGAGTGAAGG 620
QY 1774 CAGAGCAACCGGAGCTTCCAGAGGTCAGAGTGAAGTTATGTGTAAGAGTGTGCGCA 1833
DB 621 CAGAGCAACCGGAGCTTCCAGAGGTCAGAGTGAAGTTATGTGTAAGAGTGTGCGCA 680
QY 1834 ATTCACTTCTCAGAGAGGCGGATCAAGATGTGATCATCATGCTCAAGGTCAGAGGAGC 1893


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Db      ||| 421 TGTGAGGGGCGCATTCCTCCAGCGCCAGACGCTCAGAGCCTGACAGACAAAGAGGGGAGAGG 480
Qy      ||| 2071 CCCCCCGAGATCAGAGAGAGAGACCAACGTCGTCTCAGAGAGGGGCGGACCTCTCC 2130
Db      ||| 481 CCCCCCGAGATCAGAGAGAGAGACCAACGTCGTCTCAGAGAGGGGCGGACCTCTCC 540
Qy      ||| 2131 TGGCTGTCGAGGGGAGAGAGAGGCTGAGGCTTGCCAGAGGGGCGGAAATTCGCGCTGGG 2190
Db      ||| 541 TGGCTGTCGAGGGGAGAGAGAGGCTGAGGCTTGCCAGAGGGGCGGAAATTCGCGCTGGG 600
Qy      ||| 2191 AGTGTGATTCACATCCCGGTGCGGGAGGAGGAGCCCAACATCCCTTGTACAGATGA 2250
Db      ||| 601 AGTGTGATTCACATCCCGGTGCGGGAGGAGGAGCCCAACATCCCTTGTACAGATGA 660
Qy      ||| 2251 TCCCTAAGTCACTTCAGATTCGCGATATTCACAAACCTGCTTCATGAGAGTCCC 2310
Db      ||| 661 TCCCTAAGTCACTTCAGATTCGCGATATTCACAAACCTGCTTCATGAGAGTCCC 720
Qy      ||| 2311 CTCTCTCTCTAGCTTCCGCGCTCTGCGCCCTGTGAACAACCATCTGAGATCCCTGCTC 2370
Db      ||| 721 CTCTCTCTCTAGCTTCCGCGCTCTGCGCCCTGTGAACAACCATCTGAGATCCCTGCTC 780
Qy      ||| 2371 CTGCCCCCTCTCACTGCAAGTCTGAGCTGCAAGCTTCTTCCCTGACAAACGCCACAC 2430
Db      ||| 781 CTGCCCCCTCTCACTGCAAGTCTGAGCTGCAAGCTTCTTCCCTGACAAACGCCACAC 840
Qy      ||| 2431 TGACCTGAGAGGCCCAAGCTTCTCTGCTCTAGAGACTTACAAAGCTGTAGAGGCGAGGCTG 2490
Db      ||| 841 TGACCTGAGAGGCCCAAGCTTCTCTGCTCTAGAGACTTACAAAGCTGTAGAGGCGAGGCTG 900
Qy      ||| 2491 CTGCGCTGCAAGCCTGAGGGGCTCCTGAGAGAGAGGTCAATCTGATCCCTTGGGGTGGCGG 2550
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Qy      ||| 2551 GGTGGGGGTTCAGAGCCCAAGAGAGAGCACTGAGTAAATGCCCCCTGAGCTGAGAGGCC 2610
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Qy      ||| 2611 CGCCCTGCCATGAGGTTTCTCTCCCAAGAGAGAGGCGGAGGCGGAGAGAGAGAGAGAG 2670
Db      ||| 1021 CGCCCTGCCATGAGGTTTCTCTCCCAAGAGAGAGGCGGAGGCGGAGAGAGAGAGAGAG 1080
Qy      ||| 2671 GTTGGCTGCTGCTGAGGAGAGGTTCTCTCCCAAGAGAGAGGCGGAGGCGGAGAGAGAG 2730
Db      ||| 1081 GTTGGCTGCTGCTGAGGAGAGGTTCTCTCCCAAGAGAGAGGCGGAGGCGGAGAGAGAG 1140
Qy      ||| 2731 GACAGTGAAGCTGAGAGCTGCGGGGTGTGAGAGACTGAGCGGCTTCCCTCCAGAGAGC 2790
Db      ||| 1141 GACAGTGAAGCTGAGAGCTGCGGGGTGTGAGAGACTGAGCGGCTTCCCTCCAGAGAGC 1200
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Qy      ||| 2911 ATGAGTCCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2970
Db      ||| 1321 ATGAGTCCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
Qy      ||| 2971 AAGCAGCAGGTTCTCAGCCA 2990
Db      ||| 1381 AAGCAGCAGGTTCTCAGCCA 1400

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RESULT 11
 US-10-275-505-28
 ; Sequence 28, Application US/10275505
 ; Publication No. US20040081961A1
 ; GENERAL INFORMATION:

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; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DELEGANE, Angelo M.; LAL, Preeti G.
; APPLICANT: HAPALIA, April J.A.; PATTERSON, Chandra
; APPLICANT: WALIA, Narinder K.; KEARNEY, Liam
; APPLICANT: TRIBOULEY, Catherine M.; KHAN, Fatrah A.
; APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Yalda; ELIOTT, Vicki S.
; APPLICANT: NGUYEN, Daniel B.; GANDHI, Ameena R.
; APPLICANT: YANG, Junming; HERNANDEZ, Roberto
; APPLICANT: POLICKY, Jennifer L.; LU, Dyrung Aina M.
; APPLICANT: REDDY, Koopa M.; YUE, Henry
; APPLICANT: TANG, Y. Tom
; TITLE OF INVENTION: PROTEASES
; FILE REFERENCE: PI-0085 USN
; CURRENT APPLICATION NUMBER: US/10/275,505
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: PCT/US01/14651
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/209,402
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 60/207,477
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/205,803
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: 60/203,566
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 60/202,082
; PRIOR FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PERL Program
; SEQ ID NO 28
; LENGTH: 1797
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7474343CB1
US-10-275-505-28

Query Match      41.0%; Score 1233; DB 7; Length 1797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      ||| 1038 GGTCTCCACGAGCTGAGAGAGCCGCGCTACAAAGTTCAACTTCAATGCTGAGGTGGAG 1097
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Db      ||| 625 AAGATCGACAGAGCCGCTGCTCACTAGAGCTTCTCTGAGACACCCGCTGTTGGCGG 684
Qy      ||| 1158 AAGTGGCCCTGTCCAGAGGCTTGTGCTTCAATGATGACAGAGGCGGCTGATCAAC 1217
Db      ||| 685 AAGTGGCCCTGTCCAGAGGCTTGTGCTTCAATGATGACAGAGGCGGCTGATCAAC 744
Qy      ||| 1218 AATGCCACGTGTGTCCAGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1277
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Db      ||| 805 CTACAGATGGGGAATCTCTATAGAGGCAACATCAAAAGACATGCAAAAGTGGACATT 864
Qy      ||| 1338 GCCACCATCAAGATCCCAAGAAAAGCTCCCTGTGTTGTTGCTGAGTCACTCGGCC 1397
Db      ||| 865 GCCACCATCAAGATCCCAAGAAAAGCTCCCTGTGTTGTTGCTGAGTCACTCGGCC 924
Qy      ||| 1398 GACCTGCGGCTTGGGGAATTTGTGTGGCCATCGGCAATCCCTGCGCTCAAGAACCA 1457
Db      ||| 925 GACCTGCGGCTTGGGGAATTTGTGTGGCCATCGGCAATCCCTGCGCTCAAGAACCA 984
Qy      ||| 1458 GTACAAAGGAGCATGCTGAGACTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1517

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Qy 1938 GAGTCT 1997
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RESULT 14
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/ Sequence 9, Application US/09796858
/ Patent No. US20020055139A1
/ GENERAL INFORMATION:
/ APPLICANT: Holte, Douglas
/ TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING PROGNOSTIC, DIAGNOSTIC,
/ FILE REFERENCE: 7853-226-999
/ PREVENTIVE, THERAPEUTIC, AND OTHER USES
/ CURRENT APPLICATION NUMBER: US/09/796,858
/ PRIOR FILING DATE: 2001-03-01
/ PRIOR APPLICATION NUMBER: 09/223,094
/ PRIOR FILING DATE: 1998-12-30
/ PRIOR APPLICATION NUMBER: 09/223,546
/ PRIOR FILING DATE: 1998-12-30
/ PRIOR APPLICATION NUMBER: 09/224,246
/ PRIOR FILING DATE: 1998-12-30
/ PRIOR APPLICATION NUMBER: 09/312,359
/ PRIOR FILING DATE: 1999-05-14
/ PRIOR APPLICATION NUMBER: 09/336,536
/ PRIOR FILING DATE: 1999-06-18
/ PRIOR APPLICATION NUMBER: 09/342,687
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: 09/399,723
/ PRIOR FILING DATE: 1999-09-20
/ PRIOR APPLICATION NUMBER: 09/471,179
/ PRIOR FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: 09/474,071
/ PRIOR FILING DATE: 1999-12-29
/ PRIOR APPLICATION NUMBER: 09/474,072
/ PRIOR FILING DATE: 1999-12-29
/ PRIOR APPLICATION NUMBER: 09/572,002
/ PRIOR FILING DATE: 2000-05-14

/ PRIOR APPLICATION NUMBER: 09/597,993
/ PRIOR FILING DATE: 2000-06-12
/ PRIOR APPLICATION NUMBER: 09/599,596
/ PRIOR FILING DATE: 2000-06-22
/ PRIOR APPLICATION NUMBER: 09/606,565
/ PRIOR FILING DATE: 2000-06-29
/ PRIOR APPLICATION NUMBER: 09/365,164
/ PRIOR FILING DATE: 1999-07-30
/ PRIOR APPLICATION NUMBER: 09/630,334
/ PRIOR FILING DATE: 2000-07-31
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/ PRIOR FILING DATE: 2000-09-20
/ NUMBER OF SEQ ID NOS: 50
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/ ORGANISM: Mouse
/ US-09-796-858-9
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Best Local Similarity 100.0%; Pred. No. 4.5e-272; Indels 0; Gaps 0;
Matches 975; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	1601	GATCAACAGTCTCCTCTGTGGGTTCACAGCGCTGAATCCAAAGGCTGAATCTAACAGGGGCTC	1660
OY	2174	CGAATTTTCGCGCTTGGGGAGTGTGTGATTCACATTCGCGGTGTCGGGGAGGGAAAGCCCAACA	2233
Db	1661	CGAATTTTCAGCC-----TTGACCCCTTAATTTACGCTCACAGTAGAGGAAGCAGCG	1711
OY	2234	TCCCTCTGTACAGATGATTCGTGAAGATCACTTCCAAATTTCTCGGATATTCACAAAACCTG	2293
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OY	2411	CCCCCTGCACAAACGCCACACTGACCTGAGGCCGCCAGCTTCCCTCTGGCTTAGGACTTACC	2470
Db	1892	TCTTCCTGTATACAGGACTTTCCTGTACACTACAGGCTTTCATCTGTGCTCAGACACACC	1951
OY	2471	AAGCT----GTAGGCGCAGGGCTGC--TGCCTGACAGCTGGAGTCCCTGTAGAGCAGGTC	2525

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 21, 2006, 19:00:15 ; Search time 806 Seconds
(without alignments)
7917.093 Million cell updates/sec

Title: US-10-617-443b-1

Perfect score: 3006
Sequence: 1 caggagactcgaagtttcag.....gccaaaaaaaaaaaaaaaa 3006

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7204323 seqs, 1061406715 residues

Total number of hits satisfying chosen parameters: 14408646

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA_New:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

File	Score	Query Match	Length	ID	Description
1783	59.3	2551	12	US-11-186-284-78	Sequence 78, Appl
2	385	12.8	1443	US-10-821-234-613	Sequence 613, App
3	385	12.8	1894	US-11-072-512-795	Sequence 795, App
4	385	12.8	2036	US-11-091-883-91	Sequence 91, Appl
5	290.6	9.7	2476	US-11-183-914-23	Sequence 23, Appl
6	130.2	4.3	908	US-10-750-185-32084	Sequence 32084, A
7	130.2	4.3	908	US-10-750-623-32084	Sequence 32084, A
8	81.6	2.7	1497	US-10-467-657-2095	Sequence 2095, Ap
9	66.2	2.2	1446	US-10-454-437-55	Sequence 55, Appl
10	62	2.1	1376	US-10-750-185-32073	Sequence 32073, A
11	62	2.1	1376	US-10-750-623-32073	Sequence 32073, A
12	56.2	1.9	577	US-09-925-065A-873761	Sequence 873761, A
13	54.8	1.8	1102	US-10-750-185-32074	Sequence 32074, A
14	54.8	1.8	1102	US-10-750-623-32074	Sequence 32074, A
15	53.4	1.8	586	US-09-925-065A-873523	Sequence 873523, A
16	52.4	1.7	199321	US-11-121-086-10	Sequence 10, Appl
17	52.2	1.7	649	US-09-925-065A-946511	Sequence 946511, A
18	52.2	1.7	651	US-09-925-065A-949922	Sequence 949922, A
19	51.8	1.7	649	US-09-925-065A-921371	Sequence 921371, A
20	51.8	1.7	651	US-09-925-065A-928800	Sequence 928800, A

21	49.6	1.7	595	6	US-09-925-065A-829367	Sequence 829367, A
22	49.6	1.7	601	6	US-09-925-065A-766718	Sequence 766718, A
23	47.8	1.6	597	6	US-09-925-065A-907102	Sequence 907102, A
24	47.8	1.6	637	6	US-09-925-065A-74401	Sequence 74401, A
25	47.6	1.6	440	6	US-09-925-065A-257729	Sequence 257729, A
26	47	1.6	588	6	US-09-925-065A-920930	Sequence 920930, A
27	46.4	1.5	440	6	US-09-925-065A-257728	Sequence 257728, A
28	46.2	1.5	609	6	US-09-925-065A-816217	Sequence 816217, A
29	46.2	1.5	609	6	US-09-925-065A-816218	Sequence 816218, A
30	46.2	1.5	2849	9	US-11-072-512-436	Sequence 436, App
31	45.8	1.5	579	6	US-09-925-065A-118576	Sequence 118576, A
32	45.8	1.5	1992	6	US-09-925-065A-208590	Sequence 208590, A
33	45	1.5	497	6	US-09-925-065A-816219	Sequence 816219, A
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36	43.8	1.5	525	6	US-09-925-065A-669549	Sequence 669549, A
37	43.4	1.4	722	6	US-09-925-065A-168630	Sequence 168630, A
38	43.2	1.4	8888	7	US-10-933-746-41	Sequence 41, Appl
39	43.2	1.4	8888	7	US-10-933-746-41	Sequence 41, Appl
40	43	1.4	544	6	US-09-925-065A-45901	Sequence 45901, A
41	43	1.4	544	6	US-09-925-065A-45902	Sequence 45902, A
42	43	1.4	544	6	US-09-925-065A-45903	Sequence 45903, A
43	43	1.4	624	6	US-09-925-065A-669171	Sequence 669171, A
44	43	1.4	172111	12	US-11-121-086-28	Sequence 28, Appl
45	42.8	1.4	3354	9	US-11-072-512-1144	Sequence 1144, Appl

ALIGNMENTS

RESULT 1
US-11-186-284-78
Sequence 78, Application US/11186284
Publication No. US2005026493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kametkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John B.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MPM01-029P2RNM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 78
LENGTH: 2551
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (222)...(1580)
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Best Local Similarity 98.4%; Pred. No. 0;
Matches 1928; Conservative 0; Mismatches 15; Indels 16; Gaps 12;
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Qy	1218	AATGCCACGTGGTGTCCAGCAACAGTGTGCTGCCCGGAGGACAGCAGCTCAAGGTGAC	1277
Db	786	AATGCCACGTGGTGTCCAGCAACAGTGTGCTGCCCGGAGGACAGCAGCTCAAGGTGAC	845
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Db	846	CTACGAATGGGGATCTCTTATAGGCCACCATCAAAAGCATGACAAAGATCGGACATT	905
Qy	1338	GCCACCATCAAGATCATCCCAAGAAAAAGCTCCCTGATGTTGTTCTGGGTCACTCGGAC	1397
Db	906	GCCACCATCAAGATCATCCCAAGAAAAAGCTCCCTGATGTTGTTCTGGGTCACTCGGAC	965
Qy	1398	GACCTGGCGCTGGGAGTTGTGTGGCATCGGACGTCCCTTCGCCCTACAGAACCA	1457
Db	966	GACCTGGC-GCGTGGGAGTTGTGTGGCATCGG-AGTCCCTTCGCCCTACAGAACCA	1023
Qy	1458	GTGACAAAGGGGATGTGTACGACCTGCCCCAGCGGGAGGGGACGGGACCTGCGGGAC	1517
Db	1024	GTGACAAAGG--CATCTGACACTGCCAGC-GGAGGGGAGGAACTGGGCTTCGGGAC	1080
Qy	1518	TCCGACATGACCTACAT-CCAGACGGATGCCATCAT-CAACTACGGGAATCCGGGGAC	1579
Db	1081	TCCGACATGACCTACATCAGACGGATGCCATCATCAACGGAATCCGGGGAC	1140
Qy	1576	CACGTGTGAACCTGGATGGCCGAGGTTCATTTGGATCAACAACGTCMAAGTCAAGCTGGCA	1635
Db	1141	CACGTGTGAACCTGGATGGCCGAGGTTCATTTGGATCAACAACGTCMAAGTCAAGCTGGCA	1200
Qy	1636	TCTCCTTTGGCATCCCTTCAGACCGGCATCAACGGTCTCTCAAGATTTCCAGACAGC	1695
Db	1201	TCTCCTTTGGCATCCCTTCAGACCGGCATCAACGGTCTCTCAAGATTTCCAGACAGC	1266
Qy	1696	AGATCAAAAGCTGAAAGAGCGCTTCATGCGCATACGATGGCGAGTCAACCAAGCC	1755
Db	1261	AGATCAAAAGCTGAAAGAGCGCTTCATGCGCATACGATGGCGAGTCAACCAAGCC	1320
Qy	1756	TGGTGAATGAGCTGAAAGCGACCAACCGGAACTTCCAGAGGTGCGAGTGAATTTATG	1815
Db	1321	TGGTGAATGAGCTGAAAGCGACCAACCGGAACTTCCAGAGGTGCGAGTGAATTTATG	1380
Qy	1816	TGCAAGAGGTGCGCGCGAATTCACCTTCTCAGAGAGCGCGCATCCAGATGGTGCATCA	1879
Db	1381	TGCAAGAGGTGCGCGCGAATTCACCTTCTCAGAGAGCGCGCATCCAGATGGTGCATCA	1440
Qy	1876	TGCTCAAGGTCAACGGGCGTCTCTTAATGGAATCGAGTGAAGTGAAGAGGCGGTGCTGA	1935
Db	1441	TGCTCAAGGTCAACGGGCGTCTCTTAATGGAATCGAGTGAAGTGAAGAGGCGGTGCTGA	1500
Qy	1936	CCGAGTCTCTCTCTTACTGAGAGGTGCGGCGGGAGGAAGACGACTCTCTTACAGACTG	1995
Db	1501	CCGAGTCTCTCTCTTACTGAGAGGTGCGGCGGGAGGAAGACGACTCTCTTACAGACTG	1566
Qy	1996	CACCTGAGGTGTCATGTGAGGGGCGCATTCCTCCAGCGCCAAAGCTCAGAGCTTGACGA	2055
Db	1561	CACCTGAGGTGTCATGTGAGGGGCGCATTCCTCCAGCGCCAAAGCTCAGAGCTTGACGA	1620
Qy	2056	CAACGGAAGGAGCGCCCCCGCAATCAGGACGAAGGACACCGTGGTCTCTACAGAG	2115
Db	1621	CAACGGAAGGAGCG-CCCGCCGAATCAGAGCAAGAACCAACGTCGATCTCTACAGAG	1679
Qy	2116	GCGGAGGCTCTCTCTGGCTGTCCGGGACAGACGGAAGCTTGAGCTTGGCCAGGGGCCG	2175

[illegible]

Qy 1327 AGTCGGACATTGCCACCA

```

Db      646 AAGCAGACATCGACATCATCAAAATTGACACACGAGGCAAGCTGCTGCTGCTGCTG 705
Qy      1387 GTCACTCGGCGCCGACCTCGGCGCTGGGGAATTTGTGTGGCATCGGCACTCTTGCCG 1446
Db      706 GCGCGCTCCCTCAAGCTGCGCGCCGAGAGATTCTGTGTGCGCATCGGAACCCCTTTTCTT 765
Qy      1447 TACAGAACACAGTACCAAGCGGCGATGTCAGCACTGCCACGAGGAGGCGAGGAGCTG 1506
Db      766 TTCAAAACACATGACACACCGGATGTGTAGACACACCGAGGAGGCGGCAAGAGCTG 825
Qy      1507 GCCTCGGGAATCTCCGACATGATGATCAATCGATCGATCGATCAATCAATCGGAGT 1566
Db      826 GGCTCGGGAATCTCGACATGATGATCAATCGATCGATCGATCAATCAATGAGAACT 885
Qy      1567 CCGGGGAGACCATGCTGTGAACCTGGATGGGAGGTCAATGGCATCAACAGCTCAAGTCA 1626
Db      886 CCGGAGGCGCGTGTAGTAACTGGACGCTGAAGTGAATGGAATTAACATTTGAAAGTGA 945
Qy      1627 CCGCTGGCATCTCTTGCGCATCCCTCAAGACCGCATCAAGGTTCTCTCAAGAGTTCC 1686
Db      946 CAGCTGGAATCTCTTTGCAATCTCCATCTGATTAAGTTAAAGTTCTCTCAAGAGTCCC 1005
Qy      1687 AAGACAGCAGATCAAG-----ACTGGAAGAGCGCTTCATCGGCATACGAGTGC 1737
Db      1006 ATGACCGACAGGCAAGGAAAGGAAAGCATCACCAAGAAAGATTAATTTGGATCCGATGA 1065
Qy      1738 GGACGATCAACCAAGCCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1797
Db      1066 TGTCACTCACTGCTCAGCAAAAGCCAAAGAGCTGAAGAGACCGGACCTGCGCAAGAG 1125
Qy      1798 TCAGCAGTGAATTTATGTGCAAGAGGTTGCGCGCAATTCACCTTCTCAAGAGGCGGCA 1857
Db      1126 TGATCTCAGAGAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1185
Qy      1858 TCCAGATGATGATCATCATCTGTCAGAGTCAACCGGCGCTCTCTAGTGAATCGAGTGAAC 1917
Db      1186 TCAAGGAAACGACGTCATTAATCAGATCAATGACAGTCCGCGTCTCGGCAATGATG 1245
Qy      1918 TGCAGAGGCGCTGTGACCGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1977
Db      1246 TAGCAGACGTCATTAAGGAAAGGACCCCTGAACATGTGTGTCCGAGGGGTAAATGAAG 1305
Qy      1978 ACCTCCTCTTCAGCATCGACCTGAGG 2004
Db      1306 ATATCATGATCAGTGAATCCGAAAG 1332

RESULT 4
US-11-091-883-91
; Sequence 91, Application US/11091883
; Publication No. US20060024693A1
; GENERAL INFORMATION:
; APPLICANT: CIBELLI, JOSE
; APPLICANT: FERNANDEZ, EMILIO O.
; APPLICANT: JORDAO DE MEGALHAES, GUILHERME
; APPLICANT: KOCABAS, ARIF
; APPLICANT: CROSBY, JAYIER A.
; TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH
; TITLE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEBORN
; FILE REFERENCE: 53942US
; CURRENT APPLICATION NUMBER: US/11/091,883
; PRIOR APPLICATION NUMBER: 2005-03-29
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 513
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 91
; LENGTH: 2036
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-091-883-91

```

```

Query Match      12.8%; Score 385; DB 12; Length 2036;
Best Local Similarity 63.8%; Pred. No. 2,4e-81;
Matches 630; Conservative 0; Mismatches 330; Indels 27; Gaps 2;

Qy      1027 CCGCAGCGCAGGTGTCCACGACTGACAGCCGCGCTACAAAGTTCAATTCATGCTG 1086
Db      509 CTTGCGGCGCAAGGAGGAGGAAAGATCCCAACAGTTTCCGCAATTAATTAATTAATTAATTA 568
Qy      1087 AGTGTGTGAAGAAATGCCACCAAGCGGTGTCCATATGAGTCTTCTGTANACACCCGC 1146
Db      569 AGTGTGTGAAGAAATGCCCTGCGGTGTCAATGAAATGTTTGTGCAAGCTTCCGT 628
Qy      1147 TGTGTGCGCGCAACGTCGCCCTGTCCAGCGGTTCTGTCTTCATATGTCAGAGCGCGCC 1206
Db      629 TTTCTTAACGAGAGGTGCGGTGCTGATGAGGTCTGTGTTTATGTGTGCAAGATGAC 688
Qy      1207 TGATCATCAACCAATCCCAAGTGTGTCCAGCAACAGTGTGCCCCGAGCAGCAGC 1266
Db      689 TGATGTGCAAAATGCCACGTTGTGACCAAA-----GCACCGGG 730
Qy      1267 TCAGGTGAGCTTAAGAAATGGGAGCTCTATAGAGCCACCATTAAGACATCGACAA 1326
Db      731 TCAGAGTTGAGCTGAAGAACGCTGCACTTAAGAACCAAAATCAAGATGTGATGAGA 790
Qy      1327 AGTGGACATTCGACCATCAAGATCCATCCCAAGAAAAGCTCCCTGTGTGCTGG 1386
Db      791 AAGCAGACATGCTCATCTCAAAATTTGACACACAGGCAAGTGTCTGTCTGTCTG 850
Qy      1387 GTCACTCGGCGCAGCTGCGGCTGGGAGATTGTGTGTGTCATGCGAGTCTTTCGCC 1446
Db      851 GCGGCTCTCAGAGCTGCGGCGGAGAGATTGTGTGTGTCATGCGAGGCGGTTTCCC 910
Qy      1447 TACAGAACACAGTCAACAGGCAATCTGACAGTCTGCCAGCGGAGAGGCGAGGAGCTGG 1506
Db      911 TTCAAAACACAGTCAACAGGCAATCTGACAGTCTGCCAGGAGGAGGAGGAGGCTGG 970
Qy      1507 GCCTCGGGAATCTCGACATGATGATCAATCCAGAGTGTGATCAATCAATCAATCAATCA 1566
Db      971 GCTCTCGCAATCTCAAGATGATGATCAATCCAGAGTGTGATCAATCAATCAATCAATCA 1030
Qy      1567 CCGGGGAGACCATGTGTGAACCTGATGGCAGAGTATTTGATGATCAACAGCTCAAGTCA 1626
Db      1031 CCGGAGGCGCGTTAGTAAACCTGAGCGGTGAAGTATTTGAATTAACCTTTGAAGTGA 1090
Qy      1627 CCGCTGGCATCTCTTTGCGATCCCTCAGACCGGATCAACAGGTTCTCTCAAGAGTCC 1686
Db      1091 CAGCTGGAATCTCTTTGCAATCCCATGTGATTAAGTTAAAGTTCTCTCAAGAGTCCC 1150
Qy      1687 AAGCAGACATCAAG-----ACTGGAAGAGCGCTTCATCGGCATACGAGTGC 1737
Db      1151 ATGACCGACAGGCGCAAGGAAAGGACATCACCAAGAAAGATTAATTTGATTCGAATGA 1210
Qy      1738 GGACGATCAACCAAGCCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1797
Db      1211 TGTCACTCACTGCGCAAGGCAAAAGCTGAAGAGACCGGACCGGAGCTTCCAGAGC 1270
Qy      1798 TACAGAGTGAATTTATGTGCAAGGTTGGCGCCAAATTCACCTTCTCAAGAGCGCGCA 1857
Db      1271 TGATTCAGAGCGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1330
Qy      1858 TCCAGATGATGATCATCATCTGTCAGAGTCAACCGGCGCTCTCTAGTGAATCGAGTGAAC 1917
Db      1331 TCAAGGAAACGACGTCATTAATCAGATCAATGACAGTCCGTGTCTCTCCGCAATGATG 1390
Qy      1918 TGCAGAGGCGCTGTGTCAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1977
Db      1391 TCAGCAGGTATTTAAAGGAAAGCAGCTGAACATGTGTGTCCGAGGGGTAAATGAAG 1450
Qy      1978 ACCTCCTCTTCAGCATCGACCTGAGG 2004
Db      1451 ATATCATATCAAGTGAATTCGGAAG 1477

```

RESULT 5
US-11-183-914-23
Sequence 23, Application US/11183914
Publication No. US2005028214A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Guebler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Tang, Tom Y.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/183,914
FILING DATE: 19-JULY-2005
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheila
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SINITUCT01
CLONE: 2680548
US-11-183-914-23

Query Match 9.7%; Score 290.6; DB 12; Length 2476;
Best Local Similarity 57.6%; Pred. No. 5.7e-59;
Matches 577; Conservative 0; Mismatches 394; Indels 30; Gaps 2;

QY 1017 CTGGCCCTTCCCGCAGCGCTCTCCACGAGCTGAGCGCCGCGCTTACAGTTCAAC 1076
DB 445 CCGGCCGCTCTCGCCGCGCTCTAGCCGCGCCGCGCTTCTCCCGAGTCAAGTCAAC 504
QY 1077 TTGATGCTGAGCTGTGTGAGAAAGTCCGACAGCCGCTGTCACTAGAGCTCTTCTCG 1136
DB 505 TTGATGCTGAGCTGTGTGAGAAAGTCCGACAGCCGCTGTCTATATCGAATCTCTGAC 564
QY 1137 AGAGCCCGCTGTGTGAGCGCAAGTGCCTGTCCAGCGGTTCTGAGCTTCAATGATCA 1196
DB 565 CGGACACCTTTTGTGGCGCGCAGAGTCCCTATCTGAAAGGCTCAGAGATTCGTGTGCT 624
QY 1197 GAGCCCGCTGTATCATCAACCAATGCCAGTGTGTCTCAGCAAGTGTCTGCCCGGCG 1256
DB 625 GCCGATGGGCTCATGTGTACCAACGCCCATGTGTG-----GCTGAT 666

QY 1257 AGGCAGAGCTCAAGGTGACGTACAGATGGGGACTCTCTATGAGGCCACATCAAAAGC 1316
DB 667 CGGCGCAGAGTCCGTGTAGACTGTAAAGCGCGCAGATAGAGCCGTGTCAACAGT 726
QY 1317 ATCGAAGAAGTCCGACATTTGCCACATCAAGATCTCCCAAGAAAAAGCTCCCTGTG 1376
DB 727 GTGATCCCGTGTGAGACATGCGAACGCTGAGAGATTGACATGAAGAGCTCTCCCAAG 786
QY 1377 TTGTTCTGGGTCACTCGGCGGACCTGTGGGCTGGGGAGTTGTGTGCTCATCGGAGT 1436
DB 787 CTGCTCTGGGACGCTCAGCTGATGTCCGCAAGGGGAGTTGTGTGCTCATCGGAGT 846
QY 1437 CCTTGCCCTTACAGAACAGTGCACAGGCGCATGTGCAGACTGCCAGCGGAGGCG 1496
DB 847 CCTTTGACCTGCAACACATCAATCCGCGATTTGAGTCTGTCTCAGGCTCCAGCC 906
QY 1497 AGGAGCTGGGCTCCGGAAGTCCGACATGACTATCCAGACGAGATGCCATCAATCAAC 1556
DB 907 AGAGACTGTGAGCTCCCAACCAATGTGAAATTCATTAACATGATGACGCTATTGAT 966
QY 1557 TACGGAACTCCGGGGACCACTGTGAACTGTGATGCGAGGTCAATGACATCAACAG 1616
DB 967 TTTGAAACTGTGAGGTCCCTGTGTTAAGTGTGAGTGGGAGGTGATTTGAGTGAACCC 1026
QY 1617 CTGAGGTCAAGGCTGTGATCTCTTGTGCAATCCCTCAGACCGCATCAGAGTTCTTC 1676
DB 1027 ATGAAGTCAAGCTGGAATCTCTTGTGCAATCCCTTGTGATGTTCTGAGAGTTTCTG 1086
QY 1677 ACAGAGTTCGAAGACACA-----GATCAAGACTGGAAGAGCGCTTCAATC 1724
DB 1087 CATCGTGGGGAAGAAAGAAATTCCTCCCGAATCAATGGGTCCACAGGCGCTACANT 1146
QY 1725 GGCATACGATGCGGACATCAACCAAGCTGTGTGATGACTGAAGCGCAGCAACCCG 1784
DB 1147 GGGGTGATGATGCTGACCTGTGTCAGCATCTCTGTGACTACAGTTCTGAGAACCA 1206
QY 1785 GACTCCGAGAGGTGAGAGGATTTATGCAAGAGTTGGCCGGAATTCACCTCT 1844
DB 1207 AGCTTCCGAGTGTGACGATGTGTACTCATCAAAAGTATCTGTGGCTCCCTGTCA 1266
QY 1845 CAGAGAGCGGATCCAGATGTGTGATCATCTGCAAGTCAACGGGCGTCTCTAGTG 1904
DB 1267 CACCGGCTGTGTCTGCGGCTGTGTATGTGATTTGGCATTTGGGAGCAGATGTGACA 1326
QY 1905 GACTGAGTGAAGTGCAGAGGCGGTGTGACCGAGTCTCTCTCTACTGAGGTGCG 1964
DB 1327 AATGCTGAAGATGTTATGAGCTGTTCGAACCCATCCAGTTGGCAGTGCAGATCCGG 1386
QY 1965 CGGGGGAACGACAGCTCTCTTCAGCATCGACCTGAGGT 2005
DB 1387 CGGGGACGAGAAACACTGACTTATATGTGACCTCTGAGGT 1427

RESULT 6
US-10-750-185-32084
Sequence 32084, Application US/10750185
Publication No. US200502603A1
GENERAL INFORMATION:
APPLICANT: NMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: NM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922

```

; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 32084
; LENGTH: 908
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-32084

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Query Match	4.3%;	Score 130.2;	DB 8;	Length 908;
Best Local Similarity	78.4%;	Pred. No. 4.4e-21;		
Matches 156;	Conservative	0;	Mismatches 43;	Indels 0;
				Gaps 0;

OY	1358	CAAGAAAAAGCTCCCTGTGTGTTGTGCTGGGTACATCGGCGCACTCGCGGCTCGGGAGATT	141
Db	431	CCAGGAAAGCGCCCTGTGCTACTGTGTGGCCGCTCTGGAGCTGCGGCGGGAGAGTT	490
OY	1418	TGTGGTGGCCATCGGCAGTCCCTTCGCTCAAGAACACAGTGAACAAGGGCATGTCTAG	1477
Db	491	CGTGTGCGCATTTGGAAAGCCCGTTTTCCCTTCAAAACAGGCTCACACCGGGATCTCTCAG	550
OY	1478	CACTGCCCAAGCGGAGAGGCAAGGAGCTGGGCGCTCGGGGACTCGACATGGAATTACATCCA	153
Db	551	CACCAACCCAGCGTGTGGCGAAACAACTGGGGCTCCGGAACTCGGAATGGACTACATCCA	610
OY	1538	GACGGATGCGCATCATCAAC	1556
Db	611	GACAGAGCGCATCATCAAC	629

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RESULT 7
US-10-750-623-32084
Sequence 32084, Application US/10750623
Publication No. US2005028751A1
GENERAL INFORMATION:
APPLICANT: MMT GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 32084
LENGTH: 908
TYPE: DNA
ORGANISM: Bovine 19866881917166
US-10-750-623-32084

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Query Match	4.3%;	Score 130.2;	DB 8;	Length 908;
Best Local Similarity	78.4%;	Pred. No. 4,4e-21;		
Matches 156;	Conservative	0;	Mismatches 43;	Indels 0;
			Gaps	0;
QY	1358	CAGGAAAGCTCCCTGTGTGTTGTCGGGCTCACTCGGCCACTCGGCCCTCGGGAGATT	1417	
Db	411	CAAGGAAAGCTGCTGTGTACTGCTTGCCGCTCTCTCGAGCTCCGGCCCGAGAGATT	490	
QY	1418	TGTGTGGCCATTCCGCACTCCCTCGGCTTACAGAAACACAGTACCAACGGGATCGTCAG	1477	
Db	491	CGTGTCTCCATTGGAGACCCTGTTTCCCTTCAAAACAGGTCAACCAACGGGATCGTCAG	550	
QY	1478	CACCTGCCAGCGGGAGGAGCGAGCGAGCTCGGCGCTTCGGGACTTCGGAATGGAATCAATCA	153	
Db	551	CACCAACCAAGCGGTGTGGCAAAAGAACTGGAGGCTCCGGAACCTCGGACATGGAATCAATCA	610	
QY	1538	GACGGATGCATCATCAAC	1556	
Db	611	GACAGACGCATCATCAAC	629	

```

RESULT 8
US-10-467-657-2095
/ Sequence 2095, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SPA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: Seqwin99, version 1.04
/ SEQ ID NO 2095
/ LENGTH: 1497
/ TYPE: DNA
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2095

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Query Match	2.7%	Score 81.6;	DB 8;	Length 1497;
Best Local Similarity	52.8%	Pred. No. 1.6e-09;		
Matches 230; Conservative	0;	Mismatches 194;	Indels 12;	Gaps 2;

QY	1182	GGCTTCATCATGTCAAGAGCCGGCTGTATCATCAACCAATGGCCAGTGGTCCAGCAAC	1241
Db	364	GGATTGAACCTTCGGTTTCGGGCTTATCATCAACGAAAAACGGCTTCATCTCGAACCAATACC	423
QY	1242	AATGTCGCCCCGGGACAGCAGACGCTCAAGGTGACGTACGAATGGGAACTCTTATGAG	1301
Db	424	CACGTCTGTGCGCGGTATGGGGACGATCAAGAGTCTGCTCAACGACAAAGCGGAATATACC	483
QY	1302	GGCACCATCAAAAGACATGACAAAGAAATGTCGACATTCGACATCAAGATCATCCCAAG	1361
Db	484	GCCAACTCATCGTTCGATGTCCAAATCCAGATGTGCGCTCTTGAATAATGAGACGAAG	543
QY	1362	AAAAAGCTCCCTGTTGTTGTTCGTGGGTCACTTCGCGCACTTCGCGCTTGGGAACTTTGTG	1421
Db	544	GAAGACTACCGTCCTCAAAATCGGCATCCCAAAATTGMAACCGGGGAAATGGGTG	603
QY	1422	GTGGCCATCGGCAGTCCCTTCCTGCGCTTACAGAAACAAGTGAACAAGGGGATCGTAGCACT	1481
Db	604	GTCGCATTCGGCGCGCTTCCTTGCAACAGGGTACCGCGGCATTCGTGTCGC -	662
QY	1482	GCCACGGGAGGGGCAAGGAGCTGGGCGCTCCGGGACTTCGCACATGSACTACATCCAGAC	1541
Db	663	-----CAAAGGCAGAAAGCTG---CCCAAGMAAGTACACACCTTCAATCCAAAC	711
QY	1542	GATGCCATCATCAACTCAAGGAACTTCGGGGGACACATGGTGAACCTGTATGGACAGGTC	1601
Db	712	GACCTTCACATCAATCCGGGCAATTCGGGGGCGCGCTGTTCACTTAAABGACAGGTC	771
QY	1602	AATGGCATCAACAGC	1617
Db	772	GTCGGCATCAATTCG	787

RESULT 9
US-10-454-437-55
Sequence 55, Application US/10454437
Publication No. US20060277115A1
GENERAL INFORMATION:
APPLICANT: Pompeju, Markus
APPLICANT: Kroejer, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Habernauer, Gregor

```

; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
; FILE REFERENCE: BGI-128CPN
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/41031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; Remaining prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 55
; LENGTH: 1446
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1423)
; OTHER INFORMATION: RXA02630
US-10-454-437-55

Query Match
Best Local Similarity 2.2%; Score 66.2; DB 8; Length 1446;
Matches 168; Conservative 0; Mismatches 143; Indels 6; Gaps 1;

QY 1330 CGGACATTCACACATCAAGATCCCAAGAAAAGCTCCCTGTTGTTGCTGGTTC 1389
DB 747 CAGATATTGCTGTGATCAAGATTAGGAGTGTCCAACTTCAGTTAGAGCTTTGGAG 806
QY 1390 ACTGGCGGACCTGGGCGCTGGGAGTTTGTGTGCTGATCGGCACTCCCTTGGCCCTAC 1449
DB 807 ATTCGAGCGCATTAAGGCGCTTGGCAAAAGTGTGATGCTGTGTTCTCCACTGGGCTGA 866
QY 1450 AGAACAAGTGAACAAGGCGCATCTGACACTGCCAGCGGAGGCGGAGAG-----C 1503
DB 867 GCTCACTGTGTACCAACCGGATTTGTGTGCGCGGTGAACCGTCTGTGCGAGCTTCTGATG 926
QY 1504 TGGGCTCCGCGGAGCTCCGACATGACATCAATCCAGAGGATCCATCATCACTACGGGA 1563
DB 927 ATGGGAGAGAGTGTCTCCATCATGATGATCAAGCCATGCTGGATCAACCCCTGGTA 986
QY 1564 ACTCCGGGGGACCACTGCTGAACTGTGATGCGAGGCTCAATGGCATCAACAGCTCAAG 1623
DB 987 ACTGTGTGTGTCGCGTGTGATGATGATGAGCAACCTCATTTGGCATGATGCTGATATG 1046
QY 1624 TCACGGCTGGCATCTCC 1640
DB 1047 CATCATTTGAGACACC 1063

RESULT 10
US-10-750-185-32073/c
; Sequence 32073, Application US/10750185
; Publication No. US2005026063A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
```

```

; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32073
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: Bovine 19866881129851
US-10-750-185-32073

Query Match
Best Local Similarity 2.1%; Score 62; DB 8; Length 1376;
Matches 83; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1587 CTGATGCGGAGTTCATTCGATCAACAGCTCAAGTCAAGCTGCGATCTCTTGGC 1646
DB 1214 CAGGATGTGAAGTATGGAATTAAACACTGAAGGAGCAGCTGGAATCTCTTGA 1155
QY 1647 ATCCCTCAGACCGCATCAACGCTTCTCAGAGATTCCAGACAGACATCAAG 1704
DB 1154 ATTCATCTGATTAAGATTAAAGTTCTTAACGGAATCCATGACCGAACCAAG 1097
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RESULT 11
US-10-750-623-32073/c
; Sequence 32073, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32073
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: Bovine 19866881129851
US-10-750-623-32073

Query Match
Best Local Similarity 2.1%; Score 62; DB 8; Length 1376;
Matches 83; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1587 CTGATGCGGAGTTCATTCGATCAACAGCTCAAGTCAAGCTGCGATCTCTTGGC 1646
DB 1214 CAGGATGTGAAGTATGGAATTAAACACTGAAGGAGCAGCTGGAATCTCTTGA 1155
QY 1647 ATCCCTCAGACCGCATCAACGCTTCTCAGAGATTCCAGACAGACATCAAG 1704
DB 1154 ATTCATCTGATTAAGATTAAAGTTCTTAACGGAATCCATGACCGAACCAAG 1097

RESULT 12
US-09-925-065A-873761
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/ Sequence 873761, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 873761
/ LENGTH: 577
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-873761

Query Match 1.9%; Score 56.2; DB 6; Length 577;
Best Local Similarity 65.6%; Pred. No. 0.0013; Indels 0; Gaps 0;
Matches 82; Conservative 0; Mismatches 43;

QY 55 GGGCTATTCCTGCTCCATTTTTCAGATGAGTGTGAGGCCAGAGAACTGAATCT 114
DB 376 GCGTGTAGTATTCCTCCATTTTTCAGAGAGGGTTGAGGCCAGAGAGGGCGAGAGTT 435
QY 115 GTCTGAGGCCACACAGCTAGAAAGCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 174
DB 436 GCGTGAAGCCACACAGCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 495
QY 175 CCCAG 179
DB 496 CTCAG 500

RESULT 13
US-10-750-185-32074/C
/ Sequence 32074, Application US/10750185
/ Publication No. US20050260603A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: PARTIN, Dennis
/ TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-2
/ CURRENT APPLICATION NUMBER: US/10/750,185
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 32074
/ LENGTH: 1102
/ TYPE: DNA
/ ORGANISM: Bovine 19866881143159
US-10-750-185-32074

Query Match 1.8%; Score 54.8; DB 8; Length 1102;
Best Local Similarity 72.4%; Pred. No. 0.0033;
Matches 71; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
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QY 1037 AGGTCTCCACGAGCTGACGACCCCGCTACAACTTCACTTCTGACGTGTGA 1096
DB 289 AGGTGAGAAAGATCCCAACAGTCTGCGCATTAATACACTTTTTCGCATGTGGA 230
QY 1097 GAAGATCCGACGAGCGGTGTCACATAGAGCTCTCC 1134
DB 229 GAAGATGCTCTGCGGTGTCACATGAACTGTTTC 192

RESULT 14
US-10-750-623-32074/C
/ Sequence 32074, Application US/10750623
/ Publication No. US20050287531A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: PARTIN, Dennis
/ TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-1
/ CURRENT APPLICATION NUMBER: US/10/750,623
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 32074
/ LENGTH: 1102
/ TYPE: DNA
/ ORGANISM: Bovine 19866881143159
US-10-750-623-32074

Query Match 1.8%; Score 54.8; DB 8; Length 1102;
Best Local Similarity 72.4%; Pred. No. 0.0033;
Matches 71; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1037 AGGTCTCCACGAGCTGACGACCCCGCTACAACTTCACTTCTGACGTGTGA 1096
DB 289 AGGTGAGAAAGATCCCAACAGTCTGCGCATTAATACACTTTTTCGCATGTGGA 230
QY 1097 GAAGATCCGACGAGCGGTGTCACATAGAGCTCTCC 1134
DB 229 GAAGATGCTCTGCGGTGTCACATGAACTGTTTC 192

RESULT 15
US-09-925-065A-873523
/ Sequence 873523, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 873523
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LENGTH: 586
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-873523

Query Match 1.8%; Score 53.4; DB 6; Length 586;
Best Local Similarity 72.6%; Pred. No. 0.0061;
Matches 69; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Db	375	GGCTGTAGTATTCCTTCATTTTACAGAGAGGGGTTGAGGCCCGAGAGGGCGAGAAATT	434
OY	115	GTCTGAGGCCACACAGCTAGAAAGCAGCCAGGCC	149
Db	435	GCTTGAAGCCACACAGCAGCCCGAGGCCCGCC	469

Search completed: February 21, 2006, 19:51:53
Job time : 809 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, ~~using frame shift n2p model~~

Run on: February 21, 2006, 19:58:21 ; Search time 17.9 Seconds

(without alignments)
2776.794 Million cell updates/sec

Title: US-10-617-443B-1

Perfect score: 5578
Sequence: 1 caggagactcgaagtttcag.....gccaaaaaiaaaaaaaaaa 3006

Scoring table:

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-O=/abs/ABSSMB.spool/US10617443/runat.21022006.165442.15688/app.query.fasta_1
-DB=Issued_Patents_AA -QFMT=fasta -SUFFIX=n2p.rat -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=humand0.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-HOST=abss02p -USER=US10617443 @CGN 1 1 71 @runat.21022006.165442.15688
-NCPU=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSEBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_AA:*

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2: /cgn2_6/prodata/1/1aa/6 COMB.pep:*

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6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1060.5	19.0	480	2	US-09-949-016-6270 Sequence 6270, Ap
2	1053.5	18.9	480	2	US-08-923-454A-18 Sequence 18, Appl
3	1043.5	18.7	447	2	US-10-104-047-2765 Sequence 2765, Ap
4	1034.5	18.5	423	2	US-09-949-016-10514 Sequence 10514, A
5	906	16.2	458	2	US-08-923-454A-8 Sequence 8, Appl
6	903.5	16.2	458	2	US-08-923-454A-25 Sequence 25, Appl
7	903.5	16.2	458	2	US-09-008-271A-11 Sequence 11, Appl
8	903.5	16.2	458	2	US-09-968-415-11 Sequence 11, Appl
9	900.5	16.2	529	2	US-09-075-460-5 Sequence 5, Appl
10	900.5	16.1	458	2	US-08-923-454A-31 Sequence 31, Appl
11	878.5	15.7	400	2	US-09-724-864-55 Sequence 55, Appl
12	800.5	14.4	423	2	US-08-923-454A-6 Sequence 6, Appl

13	800.5	14.4	436	2	US-08-923-454A-29 Sequence 29, Appl
14	585.5	10.5	377	2	US-08-923-454A-27 Sequence 27, Appl
15	578	10.4	323	2	US-08-923-454A-4 Sequence 4, Appl
16	484	8.7	491	2	US-09-438-185A-980 Sequence 980, App
17	461	8.3	474	2	US-09-489-039A-13694 Sequence 13694, A
18	449.5	8.1	455	2	US-09-711-164-416 Sequence 416, App
19	448.5	8.0	375	2	US-09-711-164-417 Sequence 417, App
20	446	8.0	455	2	US-09-252-991A-29494 Sequence 29494, A
21	445	8.0	460	2	US-09-199-637A-132 Sequence 132, App
22	437.5	7.8	430	2	US-09-902-540-13405 Sequence 13405, A
23	432.5	7.8	499	2	US-09-673-898-6 Sequence 6, Appl
24	431	7.7	499	2	US-09-673-898-4 Sequence 4, Appl
25	429	7.7	499	2	US-09-673-898-2 Sequence 2, Appl
26	426.5	7.6	475	1	US-08-350-741-2 Sequence 2, Appl
27	426.5	7.6	475	1	US-08-463-878A-2 Sequence 2, Appl
28	426.5	7.6	477	2	US-09-543-681A-6204 Sequence 6204, Ap
29	425.5	7.6	541	2	US-08-311-731A-171 Sequence 171, Appl
30	425	7.6	474	2	US-09-689-065B-7 Sequence 7, Appl
31	424	7.6	173	2	US-08-923-454A-2 Sequence 2, Appl
32	424	7.6	414	2	US-09-388-090-6 Sequence 6, Appl
33	424	7.6	465	2	US-09-388-090-4 Sequence 4, Appl
34	423.5	7.6	409	2	US-09-902-540-11885 Sequence 11885, A
35	422.5	7.6	475	1	US-08-278-091-6 Sequence 6, Appl
36	422.5	7.6	475	1	US-08-483-859-6 Sequence 6, Appl
37	422.5	7.6	475	1	US-08-472-173-6 Sequence 6, Appl
38	422.5	7.6	475	1	US-08-487-167-6 Sequence 6, Appl
39	422.5	7.6	475	1	US-08-482-816-6 Sequence 6, Appl
40	422.5	7.6	475	1	US-08-296-149-6 Sequence 6, Appl
41	422.5	7.6	475	1	US-08-801-499-6 Sequence 6, Appl
42	422.5	7.6	475	1	US-08-615-271-6 Sequence 6, Appl
43	422.5	7.6	475	2	US-09-074-660-6 Sequence 6, Appl
44	422.5	7.6	475	2	US-09-074-660-6 Sequence 6, Appl
45	422.5	7.6	475	2	US-09-106-468-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-6270
Sequence 6270, Application US/0949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6270
LENGTH: 480
TYPE: PRT
ORGANISM: Human
US-09-949-016-6270
Alignment Scores:
Pred. No.: 2.06e-72
Score: 1060.50
Percent Similarity: 63.5%
Best Local Similarity: 49.4%
Query Match: 19.0%
DB: 2
Gaps: 12
US-10-617-443B-1 (1-3006) x US-09-949-016-6270 (1-480)
558 CCCCGCTGACACTGCTGTAGCCGAGGCTCGAGGAGACCACTGAGCCATGAGG 617

Db 48 ProGlnProGlnHisCysGluGlyAlaArgAlaArgAsp----- 60
Qy 618 AGAGGGCCAGTCTCTCTCTGTAGGGGTATTGCTGTACATGAGGGAAACAAGGCCCA 677
Db 61 -----AlaCys---GlyCysArgGluValCysGlyAlaProGluGlyAla 74
Qy 678 GGG---GAGCTAACCCGAGATCCAGCCCGGCTCATCTCCGTTGGCTCACCGCAATAT 724
Db 75 AlaCysGlyLeuGlnGluGlyProCysGlyGlyGluGlyLeuGlnCys----- 89
Qy 735 CTAACCTCTCTGTAGACCTCTGCGCCAGGCTAGACAGGGGTCCAAGTGAAGGGGGGTAGAGAA 794
Db 90 -----ValValPro-----PheGlyValProAlaSerAlaThrVal 101
Qy 795 GCCCAGACGTGGAAGGCTTTTAAACATTCGCGGGGTAGCCGAGCCCTTCCCAATGC 854
Db 102 ArgArgArgAlaGlnAlaGlyLeuCysValCysAlaSerSerGluProVal----- 118
Qy 855 CTGGTGTCACTGCACTGTGTGTGTAGGGGGTCCCAACGGGCTCAGTGTGGGCTGAG 914
Db 119 -----CysGlySerAspAlaAsnThrTyrAlaAsnLeuCysGlnLeuArg 133
Qy 915 CTGGCTCTGAACTGGGACAGGGGTCTGAGAAAGCTCTCTCTCTGCGCCACTGGGCAT 974
Db 134 AlaAla-----SerArgArgSerGluArgLeu-----His 143
Qy 975 AGGCTCTGGGAGGTGGCAGCATGTGTATCTACTATGACCTGGGCTTCCCGCCAGC 1034
Db 144 ArgPro-----ProValIleValLeuGlnArgGlyAla-----CysGly 156
Qy 1035 GCAGGTCTCCACAGCTGAGACAGCCGCGCTTACAAAGTTCAATTCATTGCTGACGTGTG 1094
Db 157 GlnGlyGlnGlnLeuArgProAsnSerLeuArgHisIleTyrAsnHelleAlaAspValVal 176
Qy 1095 GAGAAAGTGCACACAGCGGTGTGCACATAGAGCTTCTTCTGAGAACCCGCTGTTTGGC 1154
Db 177 GlnLeuIleAlaProAlaValIleAlaIleGlnLeuPheArgIleuPheProPheSerIys 196
Qy 1155 CGCAAGCTGCGCTGTCCAGAGCTTGTGCTTATCATATGTCAGAGCCGCGCTGATCATC 1214
Db 197 ArgGlnValProValAlaSerGlySerGlyPheIleValSerGlnAspGlyLeuIleVal 216
Qy 1215 ACCAATGCCACGCTGTGTGTGCAGCAACAGTGTGCCCGGCGAGCAGCTCAAGTGT 1274
Db 217 ThrAsnAlaHisValIleThrAsn-----LysHisArgValIleVal 230
Qy 1275 CAGCTACAGAAATGGGAGCTCTTATGAGGCCACATCAAGACATCGAACAAGTGGAGC 1334
Db 231 GlnLeuLysAsnGlyAlaThrTyrGlnAlaIleLysIleLysAspValAspGlnLysAlaAsp 250
Qy 1335 ATTGCCAACCTCAAGATCCATCCCAAGAAAGATCCCTGTGTGTTGCTGGGCTCATCTG 1394
Db 251 IleAlaLeuIleLysIleAspHisGlnGlyLysLeuProValIleuLeuGlyArgSer 270
Qy 1395 GCCGACCTGGCGCTGGGAGTTGTGTGGTGGCCATCGGACGTCCTTGGCTGCACAGAAC 1454
Db 271 SerGlnLeuArgProGlyGlnPheValIleAlaIleGlySerProPheSerLeuGlnAsn 290
Qy 1455 ACAAGTGAACAAGGAGCATGTGCACACTGCCACCGGAGGGGCAAGGAGTGGGCTCCGG 1514
Db 291 ThrValIleThrThrGlyIleValIleSerThrThrGlnArgGlyGlyLysGlnLeuArg 310
Qy 1515 GACTCCGACATGAGACTACATCCAGAGGATGCATATCAATCAACGGGAACTCCGGGGGA 1574
Db 311 AsnSerAspMetAspTyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGly 330
Qy 1575 CCACTGGTGAACCTGTAGTGGGAGATCATATTGGCATCAACAAGCTCAAGGTCAAGTGGC 1634
Db 331 ProLeuValAsnLeuAspGlyGlyValIleGlyIleAsnThrLeuLysValIleThrAlaGly 350
Qy 1635 ATCTCTTTGGCATCCCTTCAGACCGCATCAACGGTTCCTTCACAGATTCCAAAGCAAG 1694
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Db 351 IleSerPheAlaIleProSerAspLysIleLysPheLeuThrGlnSerHisAspArg 370
Qy 1695 CAGATCAAAAGAC-----TGGAAGAAAGCCCTTCAATCGGATACGGATGGCGACGATC 1745
Db 371 GlnAlaLysGlyLysAlaIleThrLysLysTyrIleGlyIleArgMetSerLeu 390
Qy 1746 ACAACGACCTGGTGGATGAGCTGAAAGCCAGACCAACCGGACTTCCAGAGGTCAAGCAT 1805
Db 391 ThrSerSerLysAlaLysGlnLeuLysAspArgHisAspAspPheProAspValIleSer 410
Qy 1806 GGAAATTATGTGCAAAGAGGTGCGCGGAATTACCTTCTCAGAGAGCGGCATCCAAAGT 1865
Db 411 GlnAlaTyrIleIleGlnValIleProAspThrProAlaGlnAlaGlyGlyLeuLysGln 430
Qy 1866 GGATGACATATGTCAAGTCAACGGGCTCCTCTATGACGACTCGAGTGAAGTGCAGAG 1925
Db 431 AsnAspValIleIleSerIleAsnGlyGlnSerValIleSerAlaAsnAspValSerAsp 450
Qy 1926 GCCGTGTCACCGAGTCTCTCTCTACTGAGAGTGGCGGGGAGACGACGACCTCTCTC 1985
Db 451 ValIleLysArgGlnSerThrLeuAsnMetValValArgArgGlyAsnGlnAspIleMet 470
Qy 1986 TTCAGCATCGACCTGAGGTGCTC 2009
Db 471 IleThrValIleProGluGluIle 478
RESULT 2
US-08-923-454A-18
Sequence 18, Application US/08923454A
Patent No. 6004794
GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Livi, George
APPLICANT: Karian, Eric
APPLICANT: Clinkendear, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

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; HYPOTHEtical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORIGINAL SOURCE: Feature - 213 Gly/val polymorph
US-08-923-454A-18

Alignment Scores:
Pred. No.: 7,036-72 Length: 480
Score: 1053.50 Matches: 240
Percent Similarity: 63.3% Conservative: 69
Best Local Similarity: 49.2% Mismatches: 118
Query Match: 18.9% Indels: 61
DB: 2 Gaps: 12

US-10-617-443B-1 (1-3006) x US-08-923-454A-18 (1-480)
QY 558 CCCCCCTGGACACTGCTGTGATGCCCGAGGGCTGGAGGACCACTGGACCCATGAG 617
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 48 ProGlnProGlnHicCyseGluGluYglYalArgAlaArgAsp----- 60

QY 618 AGAGGGCCAGTTCTCTCTCTGTAAAGGATTTGCTGTAGCATGAGGAAACAGAAAGGCCCA 677
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 -----AlaCys---GlyCysCyseGluValCyseGlyYalAeProGluGlyAla 74

QY 678 GGG---GGACTAACCCGAGATCCAGGCCCCGGGCTCACTCCCGTGGCTCACGGCAATAT 734
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 75 AlaCyseGlyLeuGlnGluGlyProCyseGlyGluGlyLeuGlnCys----- 89

QY 735 CTTAATCTCTCTGAGCTCTCTGCGCCAGCTGACGAGGCTCCAGTGAAGGGGGTGAAGAA 794
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 90 -----ValValPro-----PheGlyValProAlaSerAlaThrVal 101

QY 795 GCCCAGCAGCTGGAAGCCTTTTAAACATCTTCGGGGTGAAGGAGCCCTTCCCAATGC 854
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 102 ArgAArgAlaGlnAlaGluCysValCyAlaSerSerGluProVal----- 118

QY 855 CTGGTGTACATGCATGCTGTGTGGAGGGGGTCCCAACGGGCTCAGTGTGGGCTGAG 914
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 119 -----CyseGlySerAspAlaAsnThrTyAlaAsnLeuCyseGlnLeuArg 133

QY 915 CTGGCTGTGAATGGGAGACGGGGTCTCAGAAAGAGCTCTCTCTGCGCACTGGGCAT 974
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 134 AlaAla-----SerArgArgSerGluArgLeu-----His 143

QY 975 AGGCTCTGGAGGCTGGCAGCATCGTGATCTCATGTATGCACCTGGCCCTTCCCGGAC 103
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 144 ArgPro-----ProValIleValLeuGlnArgGlyAla-----CyseGly 156

QY 1035 GCAGGTCTCCACACGACTGAGCAGCCGCGGCTCAAGATTCAACTTCACTTGTGACGTGG 109
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 157 GlnGlyGlnGlnAlaAspProAsnSerLeuAlaGlnHisGlyLeuPheArgGlyLeuProPheSerLys 176

QY 1095 GAGAAGATGCAACAGCCCTGTGTCACATGAGCTTTCTGAGACACCCGCTGTTTGGC 115
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 177 GlnTySerIleAlaProAlaValAlaHisIleGlnLeuPheArgGlyLeuProPheSerLys 196

QY 1155 CGCAACGTGCCCTGTGCCAGCGGCTTGTGCTTCATCATATGCAGAGCCGCGCTGATCATC 121
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 197 ArgGluValProValAlaSerGlySerGlyPheIleValSerGluAsp**LeuIleVal 216

QY 1215 ACCATGCGCCAGCTGGTGTCCAGCAACAGTGTGCGCCCGGAGCAGAGACTCAAGTGG 127
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 217 ThrAlaAlaHisValValThrAsn-----LysHisArgValGlyVal 230

QY 1275 CAGCTTACCAATGGGCACTCTATGAGGCCAACATCAAAAGACATGCACAAAGATCGAC 133
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 231 GlnLeuTySerAsnGlyYalAlaThrTyGlnAlaTySileTyAspValAlaArgGlnTySalaAsp 250

QY 1335 ATTGGACACATCAAGATTCATCCCAAGAAAGAGCTCCGTTGTTGTGTCGGGTCACTGG 139
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 251 IleAlaLeuIleTySileAspHisGlnGlyLysGlnGlyLysLeuProValLeuLeuLeuGlyArgSer 270

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Oy	1395	GCCGACCTGGCGGCTGGGAGATTGTGATGGCCATTCGCGAGTCCCTTCGCGCTCAGAAC	1454
Db	271	SerGluLeuArgProGlyGluPheValValAlaIleGlySerProPheSerLeuGlnAsn	290
Oy	1455	ACAGTGAACACGGGCGATGTGACAGCTGCCACGGAGGGCAGGAGACTGGGCTCCGG	1514
Db	291	ThrValThrThrGlyIleValSerThrThrGlnArgGlyGlySerGluGlyLeuArg	310
Oy	1515	GACTCCGACATGGACTTACATCCAGAGGATGCCATTCATCAACTACGGGAACTCCGGGGGA	1574
Db	311	AsnSerAspMetAspTryIleGlnThrAspAlaIleLeuAsnTryGlyAsnSerGlyGly	330
Oy	1575	CCACTGTGTAACCTCGTAGTGGCAGAGTATTGGCATCAACAGCTCAAGGTTCACGCTGGC	1634
Db	331	ProLeuValAsnLeuAspGlyGlyValIleIleGlyIleAsnThrLeuValThrAlaGly	350
Oy	1635	ATCTCTTTGGCATCCCTCCAGACCGGATCACAGGTTCTCCAGAGTTCCAAAGACAG	1694
Db	351	IleSerPheAlaIleProSerAspArgIleValSerPheLeuThrGluSerHisAspArg	370
Oy	1695	CNAGTCAAGAC-----TGAAGAAGCGCTTCATCGGCATACGGAATCCGACATC	1745
Db	371	GlnAlaValSerGlyValAlaIleThrValSerValSerTryIleGlyIleArgMetSerLeu	390
Oy	1746	ACACCAAGCCCTGGTAGTAGCTGAAGCGGCAACCGGACTTCCGACAGTCAAGCAT	1805
Db	391	ThrSerSerValAlaValGluLeuValAspArgHisAspArgPheProAspValIleSer	410
Oy	1806	GGAATTTATGTGCAAGAGTTGCCGCGAATTCACCTTCTCAGAGAGCGGATCCCAAGAT	1865
Db	411	GlyAlaIleTryIleIleGluValIleProAspArgProAlaGluAlaGlyGlyLeuValSer	430
Oy	1866	GGTAGCATCATGTCAAGGTGCAACGGCGCTCTCTTAAGTGAAGTCAAGTGAAGCTGACGAG	1925
Db	431	AsnAspValIleIleSerIleAsnGlyGlnSerValValSerAlaAsnAspValSerAsp	450
Oy	1926	GCCCTGCTGACCGGAGTCTCTCTCTACTGAGAGTGGCGGGGAAACGACACTCTC	1985
Db	451	ValIleValSerGluSerThrLeuAsnMetValAlaArgArgGlyAsnGluAspIleMet	470
Oy	1986	TTTCAGCATCGCAGCTGAGGTGTC	2009
Db	471	IleThrValIleProGluGluIle	478
RESULT 3			
US-10-104-047-2765			
; Sequence 2765, Application US/10104047			
; Patent No. 6943241			
; GENERAL INFORMATION:			
; APPLICANT: HELEX RESEARCH INSTITUTE			
; TITLE OF INVENTION: NO. 6943241el full length cDNA			
; FILE REFERENCE: H1-A0105			
; CURRENT APPLICATION NUMBER: US/10/104,047			
; PRIOR FILING DATE: 2002-03-25			
; PRIOR APPLICATION NUMBER:			
; NUMBER OF SEQ ID NOS: 4096			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 2765			
; LENGTH: 447			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-104-047-2765			
Alignment Scores:			
Pred. No.:		3,94e-71	447
Score:		1043.50	241
Percent Similarity:		65.1%	72
Best Local Similarity:		50.1%	97
Query Match:		18.7%	71
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Gaps:			

OY	609	CCCATGAGAGAGGCGCCAGTCTCTCC-----TGTAAG----	641
Db	22	ProArgAaGAgSseProAlaLeuAlaLeuSerAenThrTyAlaAenLeuCySglmIn	41
OY	642	-----GGTATTCGCTGATGCATGTAGAGGGAACAGACAGAGCGGAGGGAGCTAACCCGAGAT	695
Db	42	ArgAlaGlyValArgLeuLeuArgGlyValAlaArgAlaAlaArgGlyValArgValArg----	60
OY	696	CCAGCCCCGGCCTACCTCCCGTGGGCTCACGGCAATATCTTAACCTCTCTGTAGCCTC	755
Db	61	ProAlaGlyGlyProValArgArgGlyAla-----AlaVal	72
OY	756	CTGCCCACTAGACAGGGGTCCAGTGAAGGGGGGTGAGGAAGCCAGACAGTGAAGGCTTT	815
Db	73	ArgGlyAlaLeuArgGlyAlaSerLeuGlyAlaAlaAlaAlaArg-----	88
OY	816	TTAACATTCCTCGGGGTAGCGAGGCCCTTCCAAATGCTGTGTCACTGACTGCTGT	875
Db	89	-----AlaGlyArgProLeu-----Cys	94
OY	876	GTGCTAGGGGGTCCCAACGGGCTCAAGTGTGGGCTGAGGCTGCTGTGAATCTGGAGCAGG	935
Db	95	Val-----ArgGlmIn-----LeuArgAlaAla-----	102
OY	936	GGTCTCAGGAAGAGGCTCTCTCTCTCTGAGCCACTGGGCACTGAGGAGCTGGCAGC	995
Db	103	---SerArgArgSerGluArgLeu-----HisArgPro-----	112
OY	996	ATCGTGAATCTCACTGATGCACCTGGCCCTTCCCGCAGCGCAGGTCTCCACAGCTGAGC	1055
Db	113	ProValIleValIleGlnArgGlyAla-----CysGlyGlnGlyGlnGluAspProAsn	130
OY	1056	AGCCGCGGCTCAAGTTCACATTCCTATTCCTGACGCGTGGAGGAAGATGCGACGCGGTG	1115
Db	131	SerLeuArgHisLeuPSTyrAenPheIleAlaAspValValGluLeuSileAlaProAlaVal	150
OY	1116	GTCCACATAGAGCTTTCTTGAGACACCCGCGTGTGGCGCAACGTGCCCTGTGCAGC	1175
Db	151	ValHisIleGluLeuPheArgGlyLeuProPheSerLeuArgGluValProValAlaSer	170
OY	1176	GGTTCGCTCATCATGTCAATGTCAGAGCGCGGCTGAATCATCACACATGCCAGTGTGTGC	1235
Db	171	GlySerGlyPheIleValSerGluAspGlyLeuIleValIThrAspAlaHisValValAlaThr	190
OY	1236	AGCAACAGTGTGCCCCCGGAGGAGGACAGCTCAAGGTGCAGCTCAAGATGGGAGATCC	1295
Db	191	Asn-----LysHisArgValLysValGluLeuLysAsnGlyAlaThr	204
OY	1296	TATGAGGCCACCATTAAGACATGCAACAAGATCGGACATTGCCACCATCAAGATCCAT	1355
Db	205	TyrGluAlaLysIleLysAspValAspGluLysAlaAspIleAlaLeuIleLysIleAsp	224
OY	1356	CCCAAGAAAGAGTCCCTGTGTGTGTGTGTGGGTGTCATGGCGGACCTCGGCGGGAG	1415
Db	225	HisGlnGlyLysLeuProValLeuLeuLeuLeuGlyArgSerSerGluLeuArgProGlyGlu	244
OY	1416	TTTGTGTGAGCATCGGAGATCCCTTGCSCCTTACAGAACACAGTGAACAGGGCATCGTC	1475
Db	245	PheValValAlaIleIleGlySerProPheSerLeuGlnAenThrValIThrThrGlyIleVal	264
OY	1476	AGCACTGCCACGCGGAGGAGGAGAGAGTGTGGCTCCCGGAGACTCCGACATAGATATATC	1535
Db	265	SerThrThrArgGlnArgGlyGlyLysGluLeuGlyLeuArgAenSerAspMetAspTyrIle	284
OY	1536	CAGACGATGCATCATCACTACCGGAACTCCGGGGAGCACATGTGTGAACCTGATATGC	1595
Db	285	GlnThrAspAlaIleIleAenThrCylAsnSerGlyProLeuValAsnLeuAspGly	304
OY	1586	GAGGTCAATGGCATCAACACGCTCAAGGTCAACGCTGGCATCTCTTTGGCATCCCTCA	1655
Db	305	GluValIleGlyIleAsnThrLeuLysValIThrAlaGlyIleSerPheAlaIleProSer	324

[illegible]

Db	104	gAlaIrtPLeuLaValAlaLeuGlyValGlyValAlaValLeuLeuLeuLeuTrrPglYgl	124
OY	1014	-----CACCTGGCCCTTCCCGGCAGCGCAGCTGTCCACGCTGAGCAGCCGCGG	1063
Db	124	yGlyYArgGlyProProAlaValLeuAlaAlaValProSerProProAlaSerProAr	144
OY	1064	CTACAGATTCAACCTTCATTGCTGACGTGGTGGAAAGATCGGACGCGGTGTCCATAT	1123
Db	144	gSerGlnTyrAsnPhelLeaAspValValGlnTyrThrAlaProAlaValAlaTyrTl	164
OY	1124	AGAGCTCTCTCTGAGACACCGCTGTGGCCGCAACGTGCCCTGTGCACGCTTCTGG	1183
Db	164	eGlnIleuAspArgHisProPheLeuGlyYArgGlyValProIleSerAsnGlySerG	184
OY	1184	CTTCATCATGTCCAGAGCGCGCTTCATCATCCAAATGCCACGTGGTGTCCAGACAG	1243
Db	184	yPheValValAlaAlaAspGlyLeuIleValThrAsnAlaHisValAlaAlaAsp----	202
OY	1244	TGCTGTCCCGGCGGACAGCAGCTCAAGGTGACATGACATGAGGAGGAGCTCTTAGAGC	1303
Db	203	-----ArgArgArgValArgValArgLeuLeuSerGlyAspThrTyrGlnAl	218
OY	1304	CACCATCAAGAATCGACAGAAAGTCCGACATTGCCACATCAAGATTCATCCCAAGA	1363
Db	218	aValAlaThrAlaValAlaAspProValAlaAspIleAlaThrLeuArgIleGlnThrTyrG	238
OY	1364	AAAGTCCCTGTGTGTGTGGTGGGACCTCGGCAGCCGCGCGCTGGGAGATTGTGGT	1423
Db	238	uProLeuProThrLeuProLeuGlyYArgSerAlaAspValArgGlnGlyGlnPheValVa	258
OY	1424	GGCCATCGGCAGTCCCTTGCCTTACAGAACACAGTGAACAAGGGCATGTGACGACTGC	1483
Db	258	lAlaMetGlySerProPheAlaLeuGlnAsnThrIleThrSerGlyIleValSerSerAl	278
OY	1484	CCAGCGGAGGCGCAGGAGGCTGGGCTCCGGGACCTCCGACATGACCTTCATCCGACGGA	1543
Db	278	gGlnArgProAlaAlaAspLeuGlyLeuProGlnThrAsnValGlnTyrTlEGlnThrAs	298
OY	1544	TGCCATCATCACTACGCGGAATCCGGGGGACCACTGTGTGAACCTGTGATGGCAGGTAT	1603
Db	298	pAlaAlaIleAspPheGlyAsnSerGlyGlyProLeuValAsnLeuAspGlyGlnValTl	318
OY	1604	TGGCATCAACACGCTCAAGGTGACGCGTGGCATCTTCCTTGGCATCCCTTCAGACCGCAT	1663
Db	318	eGlyValAsnThrMetLysValThrAlaGlyIleSerPheAlaIleProSerAspArgLe	338
OY	1664	CACACGGTTCCTCACAGAGTTCCAGACAGACAG-----ATCAAGAACTGGAA	1711
Db	338	uArgGlnPheLeuHisArgGlyGlyLysValAsnSerSerSerGlyIleSerGlySerCl	358
OY	1712	GAAGCGTTTCATCGGCATACGGATCGGACGATCAACCAAGCCTGTGTGATGAGCTGAA	1771
Db	358	nArgIArgTyrTlEGlyValMetMetLeuThrLeuSerProSerTlLeuAlaGlnLeuG	378
OY	1772	GGCCAGCAACCCGGACTTCCAGAGAGTGAACAGTGAATTTATGAGCAAGAGTTGGCCG	1831
Db	378	nLeuArgGlnProSerPheProAspValGlnHisGlyValLeuIleHisLysValTlIle	398
OY	1832	GAATTCACCTTTCAGAGAGCGGACATCCAAAGATGTGACATCATCGTCAAGGTCAACGG	1891
Db	398	uGlySerProAlaHisArgGlnArgGlyLeuArgProGlyAspValIleLeuAlaIleGlyG	418
OY	1892	GCGTCTCTTAAGTACGTGAGTGAAGTGAAGAGCGCTGCTGACAGCAAGTCTCTCTCT	1951
Db	418	uGlnMetValGlnAsnAlaGlnAspValTyrGlnAlaValAlaArgTrrGlnSerGlnLeuAl	438
OY	1952	ACTGAGAGTGGCGCGGGAACGACGACCTCTTTCAGCATCGACCTGAGTGAAGTGTG	2006
Db	438	aValGlnIleArgAlaGlyYArgGlnThrLeuThrLeuTyrValTrrProGlnVal	456

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1  * Sequence 25, Application US/08923454A
2  Patent No. 6004794
3  GENERAL INFORMATION:
4  APPLICANT: Creasy, Caretha
5  APPLICANT: Livi, George
6  APPLICANT: Karian, Eric
7  APPLICANT: Clinkenbeard, Helen
8  APPLICANT: Brownel, Michael
9  APPLICANT: Southan, Christopher
10 TITLE OF INVENTION: HUMAN SERINE PROTEASE
11 NUMBER OF SEQUENCES: 40
12 CORRESPONDENCE ADDRESS:
13 ADDRESSEE: Smithkline Beecham Corporation
14 STREET: 709 Swedeland Road
15 CITY: King of Prussia
16 STATE: PA
17 COUNTRY: USA
18 ZIP: 19406
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: Diskette
21 COMPUTER: IBM Compatible
22 OPERATING SYSTEM: DOS
23 SOFTWARE: FASTSEQ Version 1.5
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: US/08/923,454A
26 FILING DATE:
27 CLASSIFICATION: 435
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: 60/025436
30 FILING DATE: 06-SEPT-1996
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Baumeister, Kirk
33 REGISTRATION NUMBER: 33,893
34 REFERENCE/DOCKET NUMBER: P5047
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: 610-270-5096
37 TELEFAX: 610-270-5090
38 TELERX:
39 INFORMATION FOR SEQ ID NO: 25:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 458 amino acids
42 TYPE: amino acid
43 STRANDEDNESS: single
44 TOPOLOGY: linear
45 MOLECULE TYPE: protein
46 HYPOTHEICAL: NO
47 ANTI-SENSE: NO
48 FRAGMENT TYPE: Internal
49 ORIGINAL SOURCE:
50 US-08-923-454A-25

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Alignment Scores:	
Pred. No.:	1 9e-60
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Best Local Similarity:	45.3%
Query Match:	16.2%
DB:	2
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	Mismatches: 116
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US-10-617-443B-1 (1-3006) x US-08-923-454A-25 (1-458)

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QY 680 GGGACATACCCAGATCCAGCCCCGGGCTACTCCCGTGGCTCAGAGCAATCTCTAA 729
Db 26 GATGATGATGATProLeuIthrProAlaSerLeuIthrSer----- 41
QY 740 CCTCTCTGAGCGCTCTCTCCAGCAGGCTTCAGTGGGGGGTACGACGCCA 799
Db 42 GATThrSerAspProArgAlaArgValThrTyr-----GlyThrPro 55
QY 800 GCAAGCGAGACCTTTTATACCATTCCTGGGGTGGAGCAGCCCTTCCCAATGCTGT 858
Db 56 Ser-LeuIthrAlaArgLeuSerVal---GlyValThrIlePro---ArgAlaCysLeuThr 73

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Db      42 GlyThrSerAspProaGlaArgValThrTyr-----GlyThrPro 55
QY      800 GCAAGTGGAAAGCCTTTTAAACATTCTCGGGGTGAGGAGCCCTTCCAAATGCTGTG 859
Db      56 Ser-LeuThrPalaArgLeuSerVal---GlyValThrGluPro---ArgAlaCysLeuTh 73
QY      860 GTCACTGCACTGCGTGTGTAGGGGGTCCC---CAACGGGCTCAGTGTGGGCTGAGGCT 916
Db      73 rSer-----GlyThrProGlyProaArgAlaGluLeu-----Th 84
QY      917 GGCTCTGAACCTGGGACAGGGGTCTCAAGAAAGCCTCTCTCTGCGCCACATGCGGCTAG 976
Db      84 rAlaValaThrProaSerPheArgThrArgGluAlaSerGluAsnSerGlyThrArgSerAr 104
QY      977 G-----CCTCTGGAGAGCTGGCAGCAGTCATGTAATCTCACTAGT----- 1013
Db      104 gAlaThrLeuAlaValaAlaLeuGlyAlaGlyAlaValaLeuLeuLeuThrGlyGly 124
QY      1014 -----CACCTGGCCCTTCCCGGACAGGAGCTCTCACAGCTGACAGCCCGCG 1063
Db      124 yGlyArgGlyProProAlaValaLeuAlaAlaValaProSerProProAlaSerProAr 144
QY      1064 CTACAAGTCAACTTCATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1123
Db      144 gSerGlnTyrAsnPheIleAlaAspValaIleGluValaThrAlaProAlaValaIleTyr 164
QY      1124 AGAGCTCTCTCTGAGAACACCCGCTGTTGGCCGACAGCTGCTGCTGCTGCTGCTGCTG 1183
Db      164 eGluIleLeuAspArgIleProPheLeuGlyArgGluValaProIleSerAsnGlySerG 184
QY      1184 CTTCATCATGTCAGAGGCGCGGCTGATCATCACCAATGCCCACGCTGTGTGTCAGCAAC 1243
Db      184 yPheValaIleAlaAlaAspGlyLeuIleValaIleAsnAlaIleValaIleAsp----- 202
QY      1244 TGCTGCCCGGACGAGCAGCTCAGAGTGCAGCTACAGATGGGGACTCTATGAGGC 1303
Db      203 -----ArgArgArgValaArgValaArgLeuLeuSerGlyAspThrTyrGluAl 218
QY      1304 CACCATCAAAAGACATGCACAGAAAGTGGACATTTGCCACATCAAGTCCATCCCAAGAA 1363
Db      218 aValaIleThrAlaValaAspProValaAlaAspIleAlaThrLeuArgIleGlnThrTyr 238
QY      1364 AAAGCTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1423
Db      238 uProLeuProThrLeuProLeuGlyArgSerAlaAspValaArgGlnGlyIlePheVala 258
QY      1424 GGCCATCGGAGTCCCTTCGCTTACAGAAACAGAGTGAACAGGGCATCTGTCAGCACTGC 1483
Db      258 lAlaMetGlySerProPheAlaLeuGlnAsnThrIleThrSerGlyIleValaSerSerAl 278
QY      1484 CCAAGCGGAGGAGGAGGAGCTGGGCTCCGGGACTCCGACATGAGTACATCCAGACGA 1543
Db      278 aGlnArgProAlaArgAspLeuGlyLeuProGlnThrAsnValaGluTyrIleGlnThrAs 298
QY      1544 TGCCATCATCAAGTCAAGGAACTCCGGGGAGACCATGCTGTAACCTGGATGGCAGGCTAT 1603
Db      298 pAlaAlaIleAspPheIleAsnSerGlyGlyProLeuValaAsnLeuAspGlyIleVala 318
QY      1604 TGGCATCAACAGCTCAAGGTCAAGGCTGAGCTCTCTTTCGATCCCTCCAGACCGCAT 1663
Db      318 eGlyValaAsnThrMetLeuValaThrIleGlyIleSerPheAlaIleProSerAspArgLe 338
QY      1664 CACACGGTTCCTCAACAGAGTTCACAGACAGCAG-----ATCAAAAGCTGGA 1711
Db      338 uArgGluPheLeuIleArgGlyGlyIleTyrAsnSerSerSerGlyIleSerGlySerG 358
QY      1712 GAAGCGCTTATCGGATACGATGCGGATGCGGATCAACCAAGCGTGGATGAGCTGAA 1771
Db      358 nArgAlaGlyTyrIleGlyValaMetLeuThrLeuThrLeuSerProSerIleLeuAlaGluLeu 378
QY      1772 GGGCAGCAACCGGAGACTTCCAGAGTCAAGTGAATTTATGTGCAAGAGTTGCGCC 1831

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Db      378 nLeuArgGluProSerPheProaAspValaGlnIleGlyValaLeuIleHleValaIle 398
QY      1832 GAATTACCTTCTCAGAGAGCGGCATCCAAATGTGATCATCATCTGTAAGTCAACG 1891
Db      398 uGlySerProAlaHleArgAlaGlyLeuArgProGlyAspValaIleLeuAlaIleGly 418
QY      1892 GCGCTCTTAGTGAATCAGTGAAGTGTGAGAGAGCGCGTGTGACAGTCTCTCTCT 1951
Db      418 uGlnMetValaGlnAsnAlaGluAspValaTyrGluAlaValaArgThrGlnSerGlnLeuAl 438
QY      1952 ACTGAGGTGCGCGGGGAGACAGACACTCTTTCAGATCGACCTGAGGTG 2006
Db      438 aValGlnIleArgArgGlyArgGluThrThrThrLeuTyrValaThrProGluVal 456

RESULT 8
US-09-968-415-11
; Sequence 11, Application US/09968415
; Patent No. 6855811
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Yue, Henry
; Guejler, Karl J.
; Corley, Neil C.
; Tang, Tom Y.
; Shah, Purvi
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/968,415
; FILING DATE: 26-Sep-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/659,151
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Sheela
; REGISTRATION NUMBER: 41,201
; REFERENCE/DOCKET NUMBER: PF-0458 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SINDUCT01
; CLONE: 2680548
; SEQUENCE DESCRIPTION: SEQ ID NO: 11 :
US-09-968-415-11

Alignment Scores:
Pred. No.: 1,9e-60 Length: 458
Score: 903.50 Matches: 208
Percent Similarity: 65.1% Conservative: 91
Best Local Similarity: 45.3% Mismatches: 116
Query Match: 16.2% Indels: 44
DB: 2 Gaps: 12

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US-10-617-443B-1 (1-3006) x US-09-968-415-11 (1-458)
QY 680 GGGAGCTAACCGGAGATCCAGCCCGGCGCTCACTCCCGTGTGGCTACGGCAATATCTTAA 739
Db 26 G1yAArgAgPrOArGLeuThrProArLeuArgAlaLeu--LeuThrSer----- 41
QY 740 CCTCTCTGAGACCTCTCCGAGCCTGAGGAGGTCAGTGAAGGGGGTGAAGAACCCCA 799
Db 42 G1yThrSerAspProArGAlaArgValThrTyR-----GlyThrPro 55
QY 800 GCACGTGGAAGCCTTTTAAACATTTCCGGGTGAGCGAGCCCTTCCAAATGCTGT 859
Db 56 Ser-LeuThrAlaArgLeuSerVal--GlyValThrGluPro--ArgAlaCysLeuTh 73
QY 860 GTCACTGCACTGCTGTGTGGTGGGGGTCC--CAAGCGGCTCAAGTGTGGGCTGAGGCT 916
Db 73 rSer-----GlyThrProGluProArGAlaGlnLeu-----Th 84
QY 917 GGCTCTGAAGTGGAGCAGGGGTCTCAGAGAGAGCCTCTCTCTGCGCACTGGGCGATG 976
Db 84 rAlaValThrProArPrThArgThrArgGluAlaSerGluAAsnSerGlyThrArgSerAr 104
QY 977 G-----CCTTGGAGAGCTGGCAGCATCTGATCTCACTGATG----- 1013
Db 104 gAlaTrpLeuAlaValAlaLeuGlyAlaGlyAlaValAlaLeuLeuLeuTrpGlyG1 124
QY 1014 -----CACCTGGCCCTTCCGCGCAGCGAGGTCTCCACAGCTGAGCAGCCCGGG 1063
Db 124 yG1yArgGlyProProAlaValAlaLeuAlaValProSerProProProAlaSerProAr 144
QY 1064 CTACATCTCAATCTCATCTGATCTGAGGTGTGAGAAATCGACACAGCCGTGGTCCACAT 1123
Db 144 gSerGlnTrpArPheIleAlaAspValAlaGluTySthrAlaProAlaValAlaTyrl 164
QY 1124 AGAGCTCTTCTGAGACACCCGCTGTGGCGCGCAAGCTGGCCCTGTCCAGCGGTTCTGG 1183
Db 164 eGluLeuLeuArPArGHisProPheLeuGlyArgGluValProIleSerAsnGlySerG1 184
QY 1184 CTTCATCATGTGTAGAGCCCGGCTGATCATCATCCATGGCCACGTGGTGTCCAGCAACAG 1243
Db 184 yPheValAlaAlaAlaAspGlyLeuIleValThrAsnAlaHisValAlaAlaAsp----- 202
QY 1244 TGCTCCCGCGGCGAGCAGCAGCTCAAGGTGCGACATGAGATGGGGAATCTCATGAGGC 1303
Db 203 -----ArgArGArgValArgValArgLeuLeuSerGlyAspThrTyGluAl 218
QY 1304 CACCATCAAGAAGCATCGACAGAAGTCGGACATGGCACATCAAGATCCATCCAGAA 1363
Db 218 aValAlaThrAlaValaAspProValAlaAspIleAlaThrLeuArgG1leGlnThrG1 238
QY 1364 AAAGCTCCCTGTGTGTGTCTGGGTCACTCGGCCGACCTGGCGGCTGGGGAATTTGTGT 1423
Db 238 uProLeuProThrLeuProLeuGlyArgSerAlaAspValArgGlnGlyGluPheVala 258
QY 1424 GGCATCGGAGCTTCCCTTGGCCTTACAGAAACAGTGAACAGGGGAGATGTGAGACATCG 1483
Db 258 lAlaIleGlySerProPheAlaLeuGlnAsnThrIleThrSerGlyIleValSerSerAl 278
QY 1484 CCAGCGGAGGAGGAGGAGCTGGGCTCCGGGACTCCGACATGGAATCAATCATCAAGCGGA 1543
Db 278 aGlnArgProAlaArgAspLeuGlyLeuArgProGlnThrAsnValGluTyrlleGlnThrAs 298
QY 1544 TGCCATCATCAACTACGGGAATCTCCGGGGGAGACCATGTGTGAACCTGGATGGGAGGTCT 1603
Db 298 rAlaAlaIleAspPheGlyAsnSerGlyGlyProLeuValaAsnLeuAspGlyGluValAl 318
QY 1604 TGGCATCAACAGCTCAAGGTCAGCGGCTGGCATCTTGTGCAATCCCTGAGACGCGATG 1663
Db 318 eGlyValaAsnThrLeuValaThrAlaGlyIleSerPheAlaIleProSerAspArgLe 338
QY 1664 CACACGGTTCTCTCAGACAGTTCCAAAGCAAGCAG-----ATCAAAAGACTGGA 1711
Db 338 uArgGluPheLeuH1sArgGlyGluTybValaAsnSerSerSerGlyIleSerGlySerG1 358

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QY 1712 GAAGGCTTATCGGATACGATGCGAGCATACACCAAGCTGTGGATGAGCTGAA 1771
Db 358 nArgArGlyTrlIleGlyValaMecMetLeuThrLeuSerProSerIleLeuAlaGluLeuG1 378
QY 1772 GGCAGCAACCCGAGCTTCCAGAGGTGAGCATGGAATTTATGTGCAAGAGGTTGCCG 1831
Db 378 nLeuArgGluProSerPheProArPValGlnIleGlyValaLeuIleValaIleValaIle 398
QY 1832 GAATTCACCTTCTCAGAGAGGGGAGATCCAAATGTGTACATCTGTCAAGTCAACGG 1891
Db 398 uGlySerProAlaHisArgAlaGlyLeuArgProGlyAspValIleLeuAlaIleGlyG1 418
QY 1892 GGCTCTCAATGAGTCAAGTGAAGTGAAGGAGCGCGGTGACCCGAGTCTCTCCCT 1951
Db 418 uGlnMetValGlnaAsnAlaGluAspValTyrluAlaValaArgThrGlnSerG1leuAl 438
QY 1952 ACTGAGGTGCGCGCGGAGGAGACAGCACTCTCTTCAAGATCGCACCTGAGGTG 2006
Db 438 aValGlnIleArgArgGlyArgGluThrLeuThrLeuTyrluThrProGluVal 456

RESULT 9
US-09-075-460-5
; Sequence 5, Application US/09075460A
; Patent No. 6489136
; GENERAL INFORMATION:
; APPLICANT: Zervos, Antonio S.
; TITLE OF INVENTION: CELL PROLIFERATION RELATED GENES
; FILE REFERENCE: 10284/004001
; CURRENT APPLICATION NUMBER: US/09/075,460A
; EARLIER FILING DATE: 1998-05-08
; EARLIER APPLICATION NUMBER: US 60/046,077
; EARLIER FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 529
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-075-460-5

Alignment Scores:
Pred. No.: 2,03e-60 Length: 529
Score: 903.50 Matches: 208
Percent Similarity: 65.1% Conservative: 91
Best Local Similarity: 45.3% Mismatches: 116
Query Match: 16.2% Indels: 44
DB: 2 Gaps: 12

US-10-617-443B-1 (1-3006) x US-09-075-460-5 (1-529)
QY 680 GGGAGCTAACCGGAGATCCAGCCCGGCGCTCACTCCCGTGTGGCTACGGCAATATCTTAA 739
Db 97 G1yAArgAgPrOArGLeuThrProArPleuArgAlaLeu--LeuThrSer----- 112
QY 740 CCTCTCTGAGACCTCTCCGAGCCTGAGGAGGTCAGTGAAGGGGGTGAAGAACCCCA 799
Db 113 G1yThrSerAspProArGAlaArgValThrTyR-----GlyThrPro 126
QY 800 GCACGTGGAAGCCTTTTAAACATTTCCGGGTGAGCGAGCCCTTCCAAATGCTGT 859
Db 127 Ser-LeuThrAlaArgLeuSerVal--GlyValThrGluPro--ArgAlaCysLeuTh 144
QY 860 GTCACTGCACTGCTGTGTGGTGGGGGTCC--CAAGCGGCTCAAGTGTGGGCTGAGGCT 916
Db 144 rSer-----GlyThrProGluProArGAlaGlnLeu-----Th 155
QY 917 GGCTCTGAAGTGGAGCAGGGGTCTCAGAGAGAGCCTCTCTCTGCGCACTGGGCGATG 976
Db 155 rAlaValThrProArPrThArgThrArgGluAlaSerGluAAsnSerGlyThrArgSerAr 175
QY 977 G-----CCTTGGAGAGCTGGCAGCATCTGATCTCACTGATG----- 1013

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Db      175  gAlaTrpLeuAlaValAlaLeuGlyAlaLeuGlyAlaValLeuLeuLeuTrpGlyGly 195
QY      1014  -----CACTGGCCCTTCCCGCAGCGAGGTCTCCACCAAGTCAGACGCCGCG 1063
Db      195  yGlyArgGlyProProAlaValLeuAlaAlaValProSerProProAlaSerProAr 215
QY      1064  CTAACAAGTTCATCTTGTGCTGACGCTGGTGGAGAAATCCGACCCGCTGCTCAACAT 1123
Db      215  gSerGlnTyraenPheIleAlaSerValGlnTyraenPheIleAlaValValTyrl 235
QY      1124  AAGCTCTTCTGTGAGACCCCGCTGTTGGCCCAACGTCGCCCTGTCCAGCGCTTCTG 1183
Db      235  eGluIleLeuAraPheArgHisProPheLeuGlyArgGlyValProIleSerAanGlySerGly 255
QY      1184  CTTTCATCATGTGACAGAGCCGCGCTGATCATCACCAATGCCACGTGGTGTCCAGCAACAG 1243
Db      255  yPheValValAlaAlaAspGlyLeuIleValThrAanAlaIleValAlaAsp----- 273
QY      1244  TGTGCCCCCGGCGACAGCAGCTCAAGGTGACGTCACAGAAATGGGAGCTCTATGAGGC 1303
Db      274  -----ArgArgArgValArgValArgLeuLeuSerGlyAspThrTyrlGlnAl 289
QY      1304  CACCATCAAGAATCATGACAAAGATCGGACATTCGCACCATCAAGATCCCAAGAA 1363
Db      289  aValValIThrAlaValAspProValAlaAspIleAlaThrLeuArgIleGlnThrTyserGly 309
QY      1364  AAGCTCCCTGTGTGTGTGCTGGGTCACTGCGCGACCTGCGGCTGGGGAGTTGTGCT 1423
Db      309  uProLeuProThrLeuProLeuGlyArgSerAlaAspValArgGlnGlyGlnPheValVal 329
QY      1424  GGCATCGGACAGTCCCTGCGCTACAGAAACAGAGAACAGAGGAGGATGTCAGCATCG 1483
Db      329  lAlaMetGlySerProPheAlaLeuGlnAenThrIleThrSerGlyIleValSerSerAl 349
QY      1484  CAGCGCGAGGAGGAGGAGGAGTGGCGCTCCGCGAATCCGACATGAGTATCCAGACGA 1543
Db      349  aGlnArgProAlaArgAspLeuGlyLeuProGlnThrAenValGlnTyrlleGlnThrAs 369
QY      1544  TGGCATCATCAATCAAGGAACTCCGCGGAGCACTGCTGTAACCTGGATGGCAGGTGAT 1603
Db      369  pAlaAlaIleAspPheGlyAanSerGlyGlyProLeuValAanLeuAspGlyGlnValAl 389
QY      1604  TGGCATCAACAGCTCAAGGTCAAGGTGAGTCTGTCATCTGTCATCCCTCAGACCGGCAT 1663
Db      389  eGlyValAanThrMetLeuValThrAlaGlyIleSerPheAlaIleProSerAspArgLe 409
QY      1664  CACACCGTTCCTCAAGAGTTCCAAGACAAAGACAG-----ATCAAGACTGGAA 1711
Db      409  uArgGlyPheLeuGlnIleArgGlyGlnTyryAanSerSerSerGlyIleSerGlySerGly 429
QY      1712  GAAGCCTTCATGCGCATACGATGCGGATGCGATCACCAAGCTGGTGGATGATGATGAA 1771
Db      429  nArgArgTyrlleGlyValMetMetLeuThrLeuSerProSerIleLeuAlaIleuGln 449
QY      1772  GGCAGCAACATCCGAGCTTCCAGAGGTCAAGTGAATTAATGTCAGAAAGGTTGGGCC 1831
Db      449  nLeuArgGlyProSerPheProAspValGlnIleGlyValLeuIleHisValIlele 469
QY      1832  GAATTCACCTTCTCAAGAGCGCGCATCAAGATGTGATCATCATGCTCAAGGTCAAGCG 1891
Db      469  uGlySerProAlaGlnIleArgAlaGlyLeuArgProGlyAspValIleLeuAlaIleGly 489
QY      1892  GCGCTCTTAAGTGAATCGAGTGAAGTGAAGGCGCGTTCATCCAGAGTCTCTCTCT 1951
Db      489  uGlnMetValGlnAanAlaGlnAspValTyrlGlnAlaValArgThrGlnSerGlnLeuAl 509
QY      1952  ACTGAGAGTGGCGCGGAGGAGACAGACATCTCTTTCAGATCGACATGAGGTG 2006
Db      509  aValGlnIleArgArgGlyArgGlyuThrLeuThrLeuTyValThrProIleVal 527

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RESULT 10
US-08-923-454A-31
; Sequence 31, Application US/08923454A

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; Patent No. 6004794
; GENERAL INFORMATION:
; APPLICANT: Creasy, Caretha
; APPLICANT: Livi, George
; APPLICANT: Karian, Eric
; APPLICANT: Clinkenbeard, Helen
; APPLICANT: Browne, Michael
; APPLICANT: Southan, Christopher
; TITLE OF INVENTION: HUMAN SERINE PROTEASE
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,454A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/025436
; FILING DATE: 06-SEPT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50547
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ. ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE: 24 Xaa = Arg or Cys
; ORIGINAL SOURCE: 278 Xaa = Ala or Val
; US-08-923-454A-31

Alignment Scores:
Pred. No.: 3,22e-60 Length: 458
Score: 900.50 Matches: 212
Percent Similarity: 60.9% Conservative: 87
Best Local Similarity: 43.2% Mismatches: 121
Query Match: 16.1% Indels: 71
DB: 2 Gaps: 14

US-10-617-443B-1 (1-3006) x US-08-923-454A-31 (1-458)

QY      589  CTGAGAGGAGCAGCTGAGGCCATGAGGAGGCGCAGTTCTCTCTCT---GTAAAGGATA 645
Db      20  LeuGlyGlyIle***TrrpGly-----ArgArgProArgLeuThrProAspLeuAla 37
QY      646  TTGCTTACATGATGAGAAACAGACAGGCCCGAGGGGAGCTAACCCAGATCCAGCCCGG 705
Db      38  LeuLeu---ThrseryLthrSerAsp----- 45
QY      706  CCTCATCTCCCGTGTGCTGACGCGCAATATCTTAACCTCTCTGAGACCTCTGCGCAAGC 765
Db      46  ProArgAlaArgValThrTyrlGlyThr----- 54

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QY 766 TAGCAGGGTCAGTGAAGGGGGTGAGGAAGCCGACAGCGTGAAGCCTTTTAACATTC 825
Db 55 -----ProserLeutrP--AlaAglSerVal- 63
QY 826 TCGGGGTGAGCAGCCCTTCCCAATGCTGGTGTCACTGCACTGCTGTGTGTAAGG 885
Db 64 --GlyValThrGluPro--ArgAlaCylSerThrSer-----GlyT 76
QY 886 GTCCC---CAAGGGGTCACTGTGGGCTAGAGCTGCTCTGAACCTGGACAGGGCTCTA 942
Db 76 hrProGlyProArGlaGlnLeu-----ThzAlaValThrProArGlnThrArGTha 93
QY 943 GGAAGAGCTCCCTCCCTCCGACGAGGAGCATAG-----CCCTGGGAG 987
Db 93 rglululaserGluSerGlyThrArGSerArGAlaTrpLeuAlaValAlaLeuGlyA 113
QY 988 CTGGCAGCATCGTGAATCTCATGTATG-----CACTGGCCCTTCCG 1029
Db 113 laglyGlyAlaValLeuLeuLeuLeuLeuTrpGlyGlyAlaGlyArGlyProProAlaValLeuA 133
QY 1030 CCAAGCCAGGTTCTCCACCAAGCTGAGCAGCCGCGCTCAACAATTCAATTCTGTAGC 1089
Db 133 laAlaValProSerProProProAlaSerProArGSerGlnTyArSerPheAlaAspVal 153
QY 1090 TGGTGGAGAAATGCGACAGCGCGTGTGCACATAGAGCTTCTCCGACAGCCGCTGT 1149
Db 153 alValGlnTySerThrAlaProAlaValAlaTyrlleGluLeuSerPheAlaAspProPheA 173
QY 1150 TTGGCCGCAACGTGCCCTGTGCAGCGGTTCTGTGCTTCATGTTCAGAGCGCGCTGA 1209
Db 173 euGlyArGlnuAlProIleSerArGlySerGlyPheValAlaAlaAspGlyLeuI 193
QY 1210 TCATCAACCAATGCCCACTGTGTGTCCAGAAAGTGTGCTCCCGGAGGACAGCACTTA 1269
Db 193 leValThrSerAlaThrAlaValAlaAsp-----ArGArGArGValA 207
QY 1270 AGGTGAGCTACAGATGGGGGACTCTATAGGGCCACATCAAGAAGCATGCAAGAAGT 1329
Db 207 rglValArGLeuLeuSerGlyAspThrTyrlGlnuAlaValAlaThrAlaValAspProValA 227
QY 1330 CGACATTTGCCACCATCAAGATCCATCCCAAGAAAGCTCCCTGTGTGTGCTGGATC 1389
Db 227 laAspIleAlaThrLeuArGlyleGlnThrlySerGluProLeuProThrLeuProLeuGlyA 247
QY 1390 ACTCGCCGACCTGCGGCTGGGAGTTGTGGTGCATCGGACGTCCCTTGCCTTAC 1449
Db 247 rGSerAlaAspValArGlnGlnGlyGluPheValAlaAlaMetGlySerProPheAlaLeuG 267
QY 1450 AAGAACAAGTGAACAGGGCATCTGCAGACATGCCAGGGGAGGAGGACAGAGCTGGGC 1509
Db 267 InAsnThrIleThrSerGlyIleValSerSer**GlnArGProAlaArGAspLeuGlyL 287
QY 1510 TCCGGGACTCCGACATGACTACATCCAGACGATGCCATCACTACAGGGAATCCG 1569
Db 287 eurProGlnThrArSerValGlyTyrlleGlnThrArSerAlaAlaIleAspPheGlyAsnSerG 307
QY 1570 GGGGACCACTGTGAACCTGATGGGAGGTCAATTGGATCAACAGCTCAAGGTCAAG 1629
Db 307 lyGlyProLeuValAsnLeuAspGlyGluValIleGlyValAsnThrMetGlyValThrA 327
QY 1630 CTGGCATCTCTTGGCATCCCTCGACACGATCAACAGGTTCTCCACAGAGTCCAG 1689
Db 327 laGlyIleSerPheAlaIleProSerArGArGLeuArGluuThrArGlyGlu 347
QY 1690 ACAAGCAG-----ATCAAGAAGTGGAAAGAGCGCTTCATCGGATACGGATGC 1737
Db 347 yAlaAsnSerSerSerGlyIleSerGlySerGlnArGArGlyTyrlleGlyValMetMetL 367
QY 1738 GAGCATTCACCAAGCTGTGGATGAGCTGAAGCCCAACCCGGAATTCACAGAG 1797
Db 367 eufThrLeuSerProSerIleLeuAlaGluLeuGlnLeuArGluuProSerPheProAspV 387

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QY 1798 TCAGCAGTGAAATTTATGTGCAGAGGTGCGCCGAATTCACCTTCTCAGAGCGCGCA 1857
Db 387 alGlnHieGlyValLeuLeuLeuLeuLeuLeuLeuGlySerProAlaIleArGAlaGlyL 407
QY 1858 TCCAAGATGGTGAATCATCTGCAAGGTCAACGCGCGCTCTCTAGTGACTGAGTAC 1917
Db 407 eufArGProGlyAspValIleLeuAlaIleGlyGlnGlnMetValGlnAsnAlaGluAspV 427
QY 1918 TCAGAGGCGCGTGTGCAGCGAGTCTCTCTCTCTCTGAGAGGTGCGCGGAGGAAACGAG 1977
Db 427 alTyrlGlnuAlaValArGThrGlnSerGlnLeuAlaValGlnIleArGArGlyArGluT 447
QY 1978 ACCTCTCTTCAGATCCGACCTGAGTG 2006
Db 447 hrLeuThrLeuTyrlValThrProGluVal 456

RESULT 11
US-09-724-864-55
; Sequence 55, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; FILE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 400
; TYPE: PRF
; ORGANISM: Mouse
US-09-724-864-55

Alignment Scores:
Pred. No.: 1,446-58 Length: 400
Score: 878.50 Matches: 181
Percent Similarity: 68.0% Conservative: 63
Best Local Similarity: 50.4% Mismatches: 64
Query Match: 15.7% Indels: 52
Gaps: 4

US-10-617-443B-1 (1-3006) x US-09-724-864-55 (1-400)
QY 1069 AGTTCACTTCACTTGTCTGACGTTGTGAGAGATGCGACCCAGCGTGTCCATAGAC 1128
Db 47 SerThrThrSerSerProGlnTrpThrArGArGTrpArGArGLeuTrpSerThrCySer 66
QY 1129 TCTTCTG-----AGACAC----- 1142
Db 67 CysSerAlaAspAspArGHisThrGlySerHisThrArPLeuTyGluGluThrProSer 86
QY 1142 ----- 1142
Db 87 TrpThrGlnIleSerValAlaPheArGlyAspArGlyGlnAspGluLeuGlnAlaIleAs 106
QY 1143 -----CCGCTGTTTGGCGCAAGCTGCCCTGTCCAGCGGTTCT 1181
Db 107 LyAlaIleAspGlySerGlySerProLeuThrArGlnGlnIleProSerSerSerGlySer 126
QY 1182 GGGTTTCATATGTCAGAGCGCGGCTGTATCATCAACCAATGCCAGTGTGTCCAGAAC 1241
Db 127 GlyPheIleValSerGluAspGlyLeuIleValAlaThrAsnAlaIleValLeuThrAsn 145
QY 1242 AGTGTGCGCGCGGAGGACGAGACGACGTCAGAGTGCAGTGCAGTGCAGTGCAGTGCAG 1301
Db 146 -----GlnGlnIleValIleGlnIleValGluLeuGlnSerGlyAlaArGlyTyrlGlu 160
QY 1302 GCCACCATCAAGAAGATGCAACAGAGTGCAGATTCGCCATCAAGATCCATCCAG 1361

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QY 1184 CTTTCATGATGTCAGAGGCGCGCTGATCATCAACATGCCAGCTGGTGTCCAGCAACG 1243
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 171 yPheValValAlaAlaAspGlyLeuLeuValThrMetAlaHisValAlaAsp---- 189
QY 1244 TGCCTCCCGGCGAGGCGAGCACTCAAGGTGAGTCAAGAAATGGGACTCTATGAGGC 1303
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 190 -----ArgArgArgValArgValArgLeuLeuSerGlyAspThrTyrGluAl 205
QY 1304 CACCATCAAGACATGACACAAAGATCGGACATTGCCACATCAAGATCCCAAGAA 1363
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 205 aValValThrAlaValAspProValAlaAspIleThrLeuArgIleGlnThrIlyseI 225
QY 1364 AAGGCTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1423
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 225 uProLeuProThrLeuProLeuGlyArgSerAlaAspValArgGlnGlyLeuPheValVa 245
QY 1424 GGCATTCGCGAGCTCCCTTCGCTTACAGAACACATGACACAGGCGATGTGACGACTGC 1483
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 245 lAlaMetGlySerProPheAlaLeuGlnMetThrIleThrSerGlyIleValSerSerAl 265
QY 1484 CCAGCGGAGGCGAGGAGCTGGGCTCCGGGACTCCGACATGACTACATCCAGACGA 1543
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 265 aGlnArgProAlaArgAspLeuGlyLeuProGlnThrAsnValGluTyrIleGlnThrAs 285
QY 1544 TGCATCATCACTACGGAACCTCGGGGAGCCACTGTGGAACTG----- 1589
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 285 pAlaAlaIleAspPheGlyAsnSerIleGlyProLeuValAsnLeuAlaArgGluLeuGl 305
QY 1590 -----GATGGGAGGTCAATTGGCATCAACAGCTCAAGTCAAGCTGAG 1633
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 305 yAlaValSerLeuGlnAspGlyGluValIleGlyValAsnThrMetIleValThrAlaGl 325
QY 1634 CATTCCTCTTGGCATCCCTCCAGACCGCATCACACGCTCTTCCACAGAGTCCAAAGAA 1693
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 325 yIleSerPheAlaIleProSerAspArgLeuArgGlnPheLeuAlaArgGlyGluTyrLe 345
QY 1694 GCAG-----ATCAAGACTGGAAGAGCGCTCATCGGACTACGATGCGGAGC 1741
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 345 aAsnSerSerSerGlyIleSerGlySerGlnArgArgIleGlyValMetMetLeuThr 365
QY 1742 GATCACACCAACCTGTGTGATGATGAGCTGAAGCGCAGCAACCCGSACTTCCAGAGGTGAC 1801
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 365 rIeuSerPro----- 368
QY 1802 CAGTGAATTATGTCAGAGAGGTGGCCGAATTCACTTTCAGAGAGCGCGCATCCA 1861
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 369 -----ArgAlaGlyLeuArg 373
QY 1862 AGATGTGATCATCGTCAAGGTCAACGGGCGTCTCTAGTGAATCGAGTGAAGTGA 1921
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 373 gProGlyAspValIleLeuAlaIleGlyGlnGlnMetValGlnAsnAlaGlnAspValTyr 393
QY 1922 GGAGGCGGTGTGACCGAGTCTCTCTACTGAGAGTGGCGGGGAGAAAGCAAGCACT 1981
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 393 rGluAlaValArgThrGlnSerGlnLeuAlaValGlnIleArgArgGlyArgGluThrIle 413
QY 1982 CCTTTTCAGCATGCACTGAGGTG 2006
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 413 uThrLeuTyrValThrProGluVal 421

```

```

CORRESPONDENCE ADDRESS:
ADDRESSER: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-923-454A-29
Alignment Scores:
Pred. No.: 1,34e-52 Length: 436
Score: 800.50 Matches: 197
Percent Similarity: 59.7% Conservative: 83
Best Local Similarity: 42.0% Mismatches: 103
Query Match: 14.4% Indels: 86
DB: 2 Gaps: 14
US-10-617-443B-1 (1-3006) x US-08-923-454A-29 (1-436)
QY 680 GGAAGTAACCGAGATCCAGCCCGGCTCACTCCCTGTGTGCTACGCGCAATTATCTTA 739
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 26 GtArgArgProArgLeuThrProAspLeuArgAlaLeu-----LeuThrSer----- 41
QY 740 CCTCTCTGAGCCCTCCGCGAGCTGACAGGCTCAGTAGAGGGGGGTGAGAAAGCCCA 799
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 42 GtThrSerAspProArgAlaArgValThrTyr-----GlyThrPro 55
QY 800 GCAGCTGAAGCCTTTTAACCATTCGAGGAGTGAAGAGCCCTTCCCAATGCGCTGT 859
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 56 Ser-LeuThrPheAlaArgLeuSerVal---GlyValThrGluPro---ArgAlaCylLeuThr 73
QY 860 GTCAGTGCATGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 916
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 73 rSer-----GlyThrProGlyProArgAlaGlnLeu-----Thr 84
QY 917 GGCTCTGAAGTGAAGAGGAGTCTCAGAGAGAGCTCTCTCTGCGCCACTGGAGCATAG 976
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 84 rAlaValThrProAspThrArgThrArgGlnAlaSerGlnAsnSerGlyThrArgSerArg 104
QY 977 G-----CCTTGGAGCTGGCAGCATCTGATCTCAGTATG----- 1013
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 104 gAlaThrPheuAlaValAlaLeuGlyAlaGlyGlyValAlaValLeuLeuLeuLeuTrpGly 124

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1014 -----CACCTGGCCCTTCGCCGACGCCGAGCTCTCCACACGACTGACAGCCGCGC 1063

124 yglYArgGlyProProValValValValValProSerProProProLaseProXr 144

1064 CTACAACTTCACATCTTCATGTGACGCGTGGAGAGATCGACACGCGCTGTCCAT 1123

144 gserGlnThrAsnPhenIleAlaAspValValGluGlyGlnThrAlaProAlaValIle 164

1124 AGACCTCTCTCTGAGACACCGCTGTTGGCCGCAACGTGCCCTGTCCAGCGTTCTGG 1183

164 egluIleLeuAspArgHisProPheLeuGlyArgGluValProLisErasGlySerG 184

1184 CTTCATCATCTGCACAGGCGCGGCGATCATCATCAATGCGCACGTGTGTCCAGCAACG 1243

184 yPheValValAlaAlaAspGlyLeuIleValThrAsnAlaIleValAlaAsp----- 202

1244 TGCTCCCGCGGACAGCGACGACTCAAGTGCAGCTACAGATGGGAGATCTCTCATAGGCG 1303

203 -----ArgArgArgValArgValArgValArgLeuLeuSerGlyAspThrIleGlu 218

1304 CACCATCAAGACATCTGCACAAAGATGGGACATTTGCCACCATCAAGATCCATCCAAAGA 1363

218 aValValThrAlaValAlaAspProValAlaAspIleAlaThrLeuArgIleGlnThrArg 238

1364 AAGGCTCCCTGTGTGTGTGTGTGTGTGTCTCGGCGACCTGGCGCTGTGGGAGTTTGTGT 1423

238 uProLeuProThrLeuProLeuGlyArgSerAlaAspValArgGlnGlyLeuPheValVal 258

1424 GGCATCGGCACTCCCTTCCTCGCCCTACAAACAAGTGCACAGCGGCACTCTCAGACCTCG 1483

258 IAlaMetGlySerProPheAlaLeuGlnAsnThrIleHisSerGlyIleValSerSerAl 278

1484 CCAAGCGGAGGGCAGGAGGACTGGGCTCGGAGCTCGGACATGCAGTACATCATCCAGACGA 1543

278 aglnAsnArgProAlaArgAspLeuGlyLeuProGlnThrAsnValGlnIleGlnThrAs 298

1544 TGGCATCATCACTACCGGAACTCCGGGGGACCATGTGTAACCG-----1589

298 pAlaIleAlaLeuAspPheGlyAsnSerGlyValProLeuValAsnLeuAlaArgGluLeuG 318

1590 -----GATGCGAGGCTCATTTGGCATCAACAACGCTCAAGCTCAGCGCTCG 1633

318 yAlaValSerLeuGlnAspGlyValIleGlyValAsnThrMetCysValThrAlaG 338

1634 CATCTCTTTCGATCCCTCCAGACCGCATCAACGCTTCCTCCACAGAGTTCCAAAGCAA 1693

338 yIleSerPheAlaIleProSerAspArgLeuArgGluPheLeuHisAsArgGlyGluValS 358

1694 GCAG-----ATCAAGACTGGAAGAGAGCGCTTCATCGGCGATACCGATCGGAC 1741

358 AsnSerSerSerGlyIleSerGlySerGlnAsArgGlyIleGlyValMetMetLeuTh 378

1742 GATCACACCAAGCTGTGTGATGATGACTGAAGCGCCAGCAACCGGACTTCCAGAGTCA 1801

378 rLeuSerPro-----381

1802 CAGTGCAGAAATTATGTGCAGAGAGTTGGCGCAATTACCTTCTCAGAGAGCGGATCCA 1861

382 -----ArgAlaGlyLeuAsr 386

1862 AGATGTGATCATCATCTGCACAGGTCAACGGGCGTCTCTATGTGACTCCAGATGAGCTGA 1922

386 gProGlyAspValIleLeuAlaIleGlyGluGlnMetValGlnAsnAlaGluAspValTy 406

1922 GGAAGCCGTGCTGACCGGAGTCTCTCTTCATCTGAGAGGTGCGGCGGGGAGACGACCT 1981

406 rGluAlaValAlaArgThrGlnSerGlnLeuAlaValGlnIleArgArgGlyValArgIle 426

1982 CCTCTTCAGACCTGCAGCTGAGTGT 2006

426 uThrIleuTyValIleThrProGluVal 424

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RESULT 14
US-08-923-454A-27
? Sequence 27, Application US/08923454A
? Patent No. 6004794
? GENERAL INFORMATION:
? APPLICANT: Creasy, Caretha
? APPLICANT: Livi, George
? APPLICANT: Kattan, Eric
? APPLICANT: Clinkenbeard, Helen
? APPLICANT: Browne, Michael
? APPLICANT: Southan, Christopher
? TITLE OF INVENTION: HUMAN SERINE PROTEASE
? NUMBER OF SEQUENCES: 40
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: SmithKline Beecham Corporation
? STREET: 709 Swedeland Road
? CITY: King of Prussia
? STATE: PA
? COUNTRY: USA
? ZIP: 19406
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FastSeq Version 1.5
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/923,454A
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 60/025436
? FILING DATE: 06-SEPT-1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Baumeister, Kirk
? REGISTRATION NUMBER: 33, 833
? REFERENCE/DOCKET NUMBER: P50547
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 610-270-5096
? TELEFAX: 610-270-5090
? TELEX:
? INFORMATION FOR SEQ ID NO: 27:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 377 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? HYPOTHEICAL: NO
? ANTI-SENSE: NO
? FRAGMENT TYPE: N-terminal
? ORIGINAL SOURCE:
?
? US-08-923-454A-27
Alignment Scores:
Pred. No.:          3,14e-36      length:    377
Score:              585.50        Matches:   148
Percent Similarity: 63.9%         Conservative: 56
Best Local Similarity: 46.4%       Mismatches: 75
Query Match:        10.5%         Indels:     40
DB:                  2            Gaps:        11
US-10-617-443B-1 (1-3006) x US-08-923-454A-27 (1-377)
QY 680 GGGAAGTAAACCGAGATCCAGCCCCGGCTCACTCCGTCGTGCACAGCATATCTCTAA 739
Db 26 GtYAAGAgP-roAqgLeuthrPrOAsPlenuAlghAlenu---LeuthrSer----- 41
QY 740 CCTCTCTGTGAGCCCTCCGCCAGCCTAGACAGGCTCCAGTAGAGGGGGGTAGAGAAGCCA 799
Db 42 GlyThrSerAspProAlarValArgValThrYr-----GlyThrPro 55
QY 800 GCACGTGAAGACTTTTAACCAATTCTTCGGGGTGAGCAGACCCTTCCCAAATGCTGGT 855

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Db      56 Ser-LeuThrAlaArgLeuSerVal---GlyValThrGluPro---ArgAlaCysLeuThr 73
Qy      860 GTCACTGCACTGCTGTGTGTGGGGGTCC---CAACGGGCTCACTGTGGGCTGAGCT 916
Db      73 rSer-----GlyThrProGlyProArgAlaGlnLeu-----Th 84
Qy      917 GCGTCGAACTGGGACAGGGGATCTGAGGAAGAGCCCTCCCTCCGCGCCACGCGGATG 976
Db      84 rAlaValThrProAspThrArgThrArgGlnAlaSerGlnAsnSerGlyThrArgSerAr 104
Qy      977 G-----CCTGTGGAGCTGGCAGCATCGTATCTCACTGATG----- 1013
Db      104 gAlaThrPleuAlaValAlaLeuGlyAlaGlyAlaValLeuLeuLeuLeuThrGlyGly 124
Qy      1014 -----CACCTGGCCCTTCGCGCCAGCGCAGGATCTTCACACAGCTGACAGACGCGCG 1063
Db      124 yGlyArgGlyProProAlaValLeuAlaValProSerProProProAlaSerProAr 144
Qy      1064 CTACAAAGTTCATCTCATCTGACGTGGTGGAGAAATCGGACAGCCGCTGGTCCACAT 1123
Db      144 gSerGlnThrAsnPheIleAlaAspValAlaGlnGlyThrAlaProAlaValAlaValTyr 164
Qy      1124 AGAGCTCTTCTCTGAGACACCCGCTGTTGGCCGCAACGTGCCCTGTCCAGCGGTTCTGG 1183
Db      164 eGluIleLeuAspArgHisPheProPheLeuGlyArgGluValProIleSerAsnGlySerG 184
Qy      1184 CTTTCATCATGTGACAGGCGCGCTGATCATCACCAATGCCACGTGGTGTCCAGCAACAG 1243
Db      184 yPheValValAlaAlaAspGlyLeuIleValThrAsnAlaHisValAlaAsp----- 202
Qy      1244 TGCTGCGCGCGGCGGACGACGACGATCAAGGTGACAGATGGGGAATCCTATGAGGC 1303
Db      203 -----ArgArgArgValArgValArgLeuLeuSerGlyAspThrTyrGlnAl 218
Qy      1304 CACCATCAAGAAGCATGCAAGAAAGTGGACATTTGGCAACCATCAAGATCCCAAGAA 1363
Db      218 aValValThrAlaValAlaAspProValAlaAspIleAlaThrLeuAlaGlnIleThrLys 238
Qy      1364 AAGGCTCCCTGTGTGTGTCTGGGTGACCTGGCCGACCTGGCCGCTGGGGAAGTTGTGT 1423
Db      238 uProLeuProThrLeuProLeuGlyArgSerAlaAspValArgGlnGlyGluPheValVa 258
Qy      1424 GGCATCGGCGGACGCTTCCTGCGCTTACAGAAACAGGAAACAGGGGATGTGACAGCTGC 1483
Db      258 lAlaMetGlySerProPheAlaLeuGlnAsnThrIleThrSerGlyIleValSerSerAl 278
Qy      1484 CCAGCGGAGGAGGACGAGCTGGGCTCCGCGGACTCCGACATGGAATCATCCAGACGA 1543
Db      278 aGlnArgProAlaArgAspLeuGlyLeuProGlnThrAsnValGlyTyrIleGlnThrAs 298
Qy      1544 TGGCATCATCACTCACTGAGGAACTCGGGGGGACCACTGGTGAACCTGGATGGCGAG 1598
Db      298 pAlaAlaIleAspPheGlyAsnSerGlyGlyProLeuValAsnLeuValSerGlu 316

RESULT 15
US-08-923-454A-4
; Sequence 4, Application US/08923454A
; GENERAL INFORMATION:
; APPLICANT: Creasy, Caratha
; APPLICANT: Livi, George
; APPLICANT: Kattan, Eric
; APPLICANT: Clinkenbeard, Helen
; APPLICANT: Browne, Michael
; APPLICANT: Southan, Christopher
; TITLE OF INVENTION: HUMAN SERINE PROTEASE
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA

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; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Discrete
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,454A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/025436
; FILING DATE: 06-SEPT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50547
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 323 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-923-454A-4

Alignment Scores:
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Score: 578.00 Matches: 134
Percent Similarity: 66.7% Conservative: 46
Best Local Similarity: 49.6% Mismatches: 62
Query Match: 10.4% Indels: 28
DB: 2 Gaps: 7

US-10-617-443B-1 (1-3006) x US-08-923-454A-4 (1-323)
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Qy      885 GGTCCC---CAACGGGCTCAGGTGGGCTGAGGCTGCTGAACTGGGACAGGGGCTGC 941
Db      22 ThrProGlyProArgAlaGlnLeu-----ThrAlaValThrProAspThrArgThr 38
Qy      942 AGGAAGACCTTCCTCTCTGCTGCCCACTGGGATGAG-----CCTTGGGA 986
Db      39 ArgGlnAlaSerGlnAsnSerGlyThrArgSerArgAlaThrPleuAlaValAlaLeuGly 58
Qy      987 GCTGGCAGCATGTGATCTCACTGATG-----CACCTGGCCCTTCCC 1028
Db      59 AlacGlyAlaValLeuLeuLeuLeuThrGlyGlyArgGlyProProAlaValLeu 78
Qy      1029 GCCAGCGAGGTCTCCACACAGCTGACGCGCGGCTCAAGTTCAATTCATGCTGAC 1088
Db      79 AlaAlaValProSerProProProAlaSerProAspSerGlnTyrAsnPheIleAlaAsp 98
Qy      1089 GTGTGGAGAAATGCAACAGCCGTGTGCAATAGACTCTTCTGAGACACCCGCTG 1148
Db      99 ValValGlyGlyThrAlaProAlaValAlaValTyrIleGluIleLeuAspArgHisProHe 118
Qy      1149 TTTGGCCGCAACGTGCGCTGTCTGACAGCGGTTGTGCTTCATCATGTCAAGAGCGGCTG 1208
Db      119 LeuGlyArgGluValProIleSerAsnGlySerGlyPheValAlaAlaAlaAspGlyLeu 138
Qy      1209 ATCATCAACCAATGCCCAAGTGTGTCCAGCAAGTGTGCCCGCGGACAGGACAGCTC 1268

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GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 21, 2006, 20:45:26 ; Search time 83.2 Seconds
(without alignments)
3019.219 Million cell updates/sec

Title: US-10-617-443B-1

Perfect score: 5578
Sequence: 1 caggagaccgcgaagttgcag.....gccaaaaaaaaaaaaaa 3006

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pro -NOR=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs802p
-USER=US10617443 @CGN 1.1 307 @runat 21022006.165448.15797 -NCPU=6 -ICPU=3
-NO_WMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: Published Applications AA.Main:*
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3: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubppaa/US10A_PUBCOMB.pep:*
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6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1679	30.1	334	US-10-189-099A-2	Sequence 2, Appl1
2	1679	30.1	334	US-10-617-443B-2	Sequence 2, Appl1
3	1668	29.9	453	US-09-796-753-32	Sequence 12, Appl1
4	1668	29.9	453	US-10-275-505-14	Sequence 34, Appl1
5	1668	29.9	453	US-10-381-820A-8	Sequence 8, Appl1
6	1668	29.9	453	US-10-485-313A-33	Sequence 33, Appl1
7	1668	29.9	453	US-11-140-224-14	Sequence 14, Appl1
8	1638	29.4	459	US-09-796-753-34	Sequence 34, Appl1
9	1554	27.9	452	US-10-485-313A-27	Sequence 27, Appl1
10	1546.5	27.7	452	US-10-301-822-79	Sequence 79, Appl1
11	1378	24.7	286	US-09-764-898-256	Sequence 256, Appl1

12	1150	20.6	357	US-10-485-313A-34	Sequence 34, Appl1
13	1121	20.1	330	US-09-764-898-184	Sequence 184, Appl1
14	1075	19.3	363	US-10-485-313A-39	Sequence 39, Appl1
15	1060.5	19.0	480	US-10-170-385-355	Sequence 355, Appl1
16	1060.5	19.0	480	US-10-172-636-48	Sequence 48, Appl1
17	1054.5	18.9	517	US-10-264-049-2310	Sequence 2310, Appl1
18	1043.5	18.7	447	US-10-104-047-2765	Sequence 2765, Appl1
19	1000	17.9	405	US-09-925-298-552	Sequence 552, Appl1
20	1000	17.9	405	US-10-102-806-552	Sequence 552, Appl1
21	903.5	16.2	458	US-09-968-415-11	Sequence 11, Appl1
22	903.5	16.2	458	US-10-197-634-11	Sequence 11, Appl1
23	903.5	16.2	458	US-10-180-719-11	Sequence 11, Appl1
24	903.5	16.2	458	US-10-352-684A-10	Sequence 10, Appl1
25	903.5	16.2	458	US-11-045-577-11	Sequence 11, Appl1
26	903.5	16.2	529	US-10-216-667-5	Sequence 5, Appl1
27	902	16.2	476	US-09-935-390A-37	Sequence 37, Appl1
28	902	16.2	476	US-10-789-241-50	Sequence 50, Appl1
29	902	16.2	476	US-10-772-636-8	Sequence 8, Appl1
30	886	15.9	325	US-10-730-476A-44	Sequence 44, Appl1
31	886	15.9	325	US-10-730-476A-44	Sequence 44, Appl1
32	882	15.8	321	US-10-730-476A-52	Sequence 52, Appl1
33	882	15.8	321	US-10-730-476A-52	Sequence 52, Appl1
34	866	15.5	325	US-10-730-476A-45	Sequence 45, Appl1
35	866	15.5	325	US-10-730-476A-47	Sequence 47, Appl1
36	866	15.5	325	US-10-730-476A-47	Sequence 47, Appl1
37	866	15.5	325	US-10-730-476A-45	Sequence 45, Appl1
38	866	15.5	325	US-10-730-476A-46	Sequence 46, Appl1
39	866	15.5	325	US-10-730-476A-47	Sequence 47, Appl1
40	862	15.5	325	US-10-730-476A-53	Sequence 53, Appl1
41	862	15.5	325	US-10-730-476A-53	Sequence 53, Appl1
42	854	15.3	178	US-09-969-384-18	Sequence 18, Appl1
43	696	12.5	225	US-10-730-476A-48	Sequence 48, Appl1
44	696	12.5	225	US-10-730-476A-48	Sequence 48, Appl1
45	692	12.4	210	US-10-730-476A-62	Sequence 62, Appl1

ALIGNMENTS

RESULT 1
US-10-189-099A-2
; Sequence 2, Application US/10189099A
; Publication No. US20040005659A1
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew L
; APPLICANT: Oi, Jian-shen
; APPLICANT: Chen, Cailin
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Human PRSS-11 like S2 serine protease and uses thereof
; FILE REFERENCE: ORT-1644
; CURRENT APPLICATION NUMBER: US/10/189,099A
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 334
; TYPE: PRT
; ORGANSIM: Homo sapiens
US-10-189-099A-2

Alignment Scores:

Pred. No.: 7,486-98
Score: 1679.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 30.1%
DB: 4
Length: 334
Matches: 334
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-617-443B-1 (1-3006) x US-10-189-099A-2 (1-334)

QY 1011 ATGACCTGGCCCTTCGGCCAGCCAGGTCTTCACACGACTGACAGCCCGGCTTACAG 1070
DB 1 MetH1SeuH1AlaLeuProAlaSer1aGlyLeuH1SgIntLeuSerProArgTyr1ys 20

Dd		232	sliEhiSProlYsblySvlsPleuProValleuLeuLcuLyhiSBserlAabPleuAqPr	252
Oy		1409	TGGGAGATTGTGTGGCCATCGCAGTCCCTTCGCCCTACAGAACAAGTGAACAACGGG	1468
Dd		252	oGlYgluhPeVAlValAlAlIegLYseRProPhelAlaleuGlnAbenThrValThrThngl	272
Oy		1469	CATGCTCAAGCACTGCCACCGGAGAGGCAGAGGACTGGGCTCCGGGACTCCGACATGGA	1528
Dd		272	yileValseRThralagInArsgLuNgLYARgLUeudLYleuWrgApSeAPMeLas	292
Oy		1529	CTACATCCAGACGGATGGCATCATCAATCAACGGAACTCCGGGGAGCAACTGTGAACCT	1588
Dd		292	pTYrlleGlnThraPalAlIellAsenTyRGlyAmSerolYglYPProLeuValAsnue	312
Oy		1589	GGATGGCAGGTCATTGGCATCAACAACGCTCAAGGTCAACGCTGGCATCTCTTTGCCAT	1648
Dd		312	uASpOlYglUVallllegLYlleaenThrleuYsValThrhlagLYlleSeRphenAlAlI	332
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Dd		332	eProSeRaSParlgIleThraRgPheLeuthRcluhPegInAsPySGlnIlleYsAsPTr	352
Oy		1709	GAGAGAGGCTTCATCGGCATACGGATGCGGACGATCAACACAGCCGtGNGATTAAGCT	1768
Dd		352	PlyeYsaRgPheIIegLYlleAgMwaIRgThrlleThrProSeRleuVaIAABgLUle	372
Oy		1769	GAAGGCCAGCAACC CGGACTTCCCGAGAGTGACAGCTGGAATTTATGTGCAAGAGTTGC	1828
Dd		372	uLYsAlaseRnaRPromPaBpeRogluVAIseserclYlleTyRValGlnGUValAl	392
Oy		1829	GCCGAATTCACCTTTCTCAAGAGCGCGCATCCAGATGCTGAATCATCATGCTCAAGTCAA	1888
Dd		392	aProAmSeRProSeRgInArsgLYglYLleGlnAspLYlaPleIIleValLYsValAs	412
Oy		1889	CGGGCGTCTCTMAAGTGAAGCTGAGAGTGAAGTGAAGAGGCGtGtGCAACGAGTCTCCTCT	1948
Dd		412	nGIYArsProLeuValAsPseSeRgLUeugInmUlAvallAuThrgUsseRProLe	432
Oy		1949	CCTACTGAGAGTGC GCGCGGGGAAACGACGACTCCTCTTCAGCATCGCAGCTGAGTGTG	2008
Dd		432	uLeuLcuGluValInArGaRgGYlaenAsPleuLeuPheSerIIeaIaProgIUValVa	452
Oy		2009	CATG 2012	
Dd		452	Imet 453	
 RESULT 4 US-10-275-505-14 ; Sequence 14, Application US/10275505 ; Publication No. US20040081961AI ; GENERAL INFORMATION: ; APPLICANT: INCYTE GENOMICS, INC. ; APPLICANT: DELEGANE, Angelo M.; LAL, Preeti G. ; APPLICANT: HARALIA, April U.A.; PATTERSON, Chandra ; APPLICANT: WALIA, Nairinder K.; KEANEY, Liam ; APPLICANT: TRIBOULEY, Catherine M.; KHAN, Farrah A. ; APPLICANT: YAO, Monique G.; BAUGHN, Mariah R. ; APPLICANT: AZIMZAI, Yalda; ELLIOTT, Vicki S. ; APPLICANT: NGUYEN, Dannel B.; GAUDIT, Aneena R. ; APPLICANT: YANG, Junning; HERNANDEZ, Roberto ; APPLICANT: POLICKY, Jennifer L.; LU, Dyrung Alina M. ; APPLICANT: REDDY, Roopa M.; YUE, Henry ; APPLICANT: TANG, Y. Tom ; TITLE OF INVENTION: PROTEASES ; FILE REFERENCE: PI-0085 USN ; CURRENT APPLICATION NUMBER: US/10/275_505 ; CURRENT FILING DATE: 2002-11-04 ; PRIOR APPLICATION NUMBER: PCT/US01/14651 ; PRIOR FILING DATE: 2001-05-04 ; PRIOR APPLICATION NUMBER: 60/209,402 ; PRIOR FILING DATE: 2000-06-01 ; PRIOR APPLICATION NUMBER: 60/207,477 ; PRIOR FILING DATE: 2000-05-25				

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      / PRIOR APPLICATION NUMBER: 60/205,803
      / PRIOR FILING DATE: 2000-05-17
      / PRIOR APPLICATION NUMBER: 60/203,566
      / PRIOR FILING DATE: 2000-05-11
      / PRIOR APPLICATION NUMBER: 60/202,082
      / PRIOR FILING DATE: 2000-05-04
      / NUMBER OF SEQ ID NOS: 28
      / SOFTWARE: PERL Program
      / SEQ ID NO 14
      / LENGTH: 453
      / TYPE: PRT
      / ORGANISM: Homo sapiens
      / FEATURE:
      / NAME/KEY: misc_feature
      / OTHER INFORMATION: Inctye ID No: 7474343CD1
US-10-275-505-14

Alignment Scores:
Pred. No.:          3,97e-97           Length:         453
Score:             1668.00            Matches:         354
Percent Similarity: 79.0%              Conservative:    11
Best Local Similarity: 76.6%            Mismatches:     30
Query Match:       29.9%                Indels:         67
DB:               4                    Gaps:          7

US-10-617-443B-1 (1-3006) x US-10-275-505-14 (1-453)

QY   749  GAGCCTCGTCCGACCATGAGCAAGGTTCAGTGAGGGGGGTGAGGAAGCCGACAGTGA  808
      |||||.....|||
Db   19  GIUProAlaIaIaPro-----CyEProAlaIaIaGcys  29
      .....

QY   809  AGCCTTTTAAACATTCTCGGGGTGAGCGAGCCCTTCC-----CAA  850
      ::::|
Db   30  AspaI-----SerArgCysProSerProArgCysProGIyGIlytyr  43
      .....

QY   851  ATGCCTGGTGCATCTGCATCTGTGTGTGA-----CG  883
      :::||:::|||||:|||||
Db   44  ValProAspleu-CysAnCysCyLeuValCyEAlaIaSerGIuGIuProCysgl  63
      ..|||..|:::|||||

QY   884  GGGGCCCAACGGGCTCAGTGGGCTGAGGCTG-----GCTCT  922
      |||||:::|||||
Db   63  yGIProleuAspeirProcysgIyGIuSerleuGlucyValaIaArgIyleuCysAtgCy  83
      .....

QY   923  GAACCTGGGACAGGGGCTCTC-----  941
      |||:::
Db   83  sArGTripserHisAlaValCysgIyThraSprGIyHieThrTyrlaAenValCyAlaIe  103
      .....

QY   942  -----AGGAAGACCTTCCTCTCTGCCCCATGGGCAATAGCCTTGGGAGC  988
      .....
Db   103 uGIAlaIaSerArxArgAlaIeGIuGIuSerIdIyThrProValaIaArgIuIeGIuLy  123
      .....

QY   989  TGGGAGCATGTGATCTCATCTGATGAGCACCTGGCCCTCCGCGACGGAGGTCACCA  1046
      |||||:::
Db   123 sgIyAlaCyAsProIeu-----GIyleuHieGI  132
      .....

QY   1049 GCTGAGCAGCCCGGCTTAACAATTCAATTCCTGACSCGTGTGTGAAGAATGCAAC  1108
      .....
Db   132 nIeuSerSerProArgrTyrlYsPheAenPhelIaIaAspValaIGluYsIIeaIaPr  152
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QY   1109 AGCCGTGTCACATAGACTCTTTCCTGTAGACACCCTGTTTGGCCGCAACGTGCCCT  1166
      .....
Db   152 cAlaValaIHisIleGIuIeuPhelEuArgHIaProIeuHeGIaIaArgAenValProIe  172
      .....

QY   1169 GTCCAGCGGTTCTGGCTTATCATGATGACAGGCGGCGCTATCATCAACATGGCCACGT  1222
      .....
Db   172 uSerSerIySerGIyPheIIeueISerGIuIEGIyleuIleIetrnAenAlaHIsVa  192
      .....

QY   1229 GGTTCCAGCAACAGTGTGCTGCCCGGGGAGGACACAGCTCAAGGTGACGTACAGAAATG  1288
      .....
Db   192 IValISerSerAmberAlaIaIaProGIyArGIInGIuIeuYsValaIGIuIeGIuInaEnGI  212
      .....

QY   1289 GGACTCTCTATGAGGCCAACATCAAGACATTCGACAAAGAAGTCCGACATTCGCCACCATCA  1346
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Db	212	YASPSERYTRGWLIAETHRIILEYAAAPLIEAPLYSLYSSERAPPLIEALITHRIILEY	232
QY	1349	GATCCATCCCAAGAAAAGCTCCCTGTGTGTGTGCTGGGTCACTGGCCGACCTGGGCC	1408
Db	232	SILEHISPROLYSLYSLYBLEUPROVALLEULEULEUGLHISERIALAPLEUABGR	252
QY	1409	TGGGAGATTTCGTGTGGCCATTCGGCAGTCCCTTCGCCCTACAGAACACAGTGAACAAGG	1468
Db	252	OGLYGIUPEVALVALAIAIEGLYISERPROHEALIEUGINASTHVALTHTRCI	272
QY	1469	CATCGTCAGACTGCCAGCGGAGGAGGAGGAGAGTGGGCTCCGGGACCTCCGACATGGA	1528
Db	272	YLIEVALSERTHRALAGINAGGLUGLYARGLEULEUGLYLEUWAGPSERASPMEDAS	292
QY	1529	CTACATCCAGACGAGTGCATCATCACTAACCTACCGGAACTCCGGGGACCACTGTGAACCT	1588
Db	292	PTYRILEGINTHRAPALAIETIEASNTYRGLYASNSERGLYGLYPROLEUVALASME	312
QY	1589	GGATGCGCAGGTCATTGGCATTAACCGTCAAGGTCACGGCTGGCATTCCTTTGCCAT	1644
Db	312	UASPELYGIUVALIIEGLYILEASNTHLEULYSVALTHRALAGYIIIESERPHALAI	332
QY	1649	CCCCGACGCGCATCAACGCGTTCCTCAAGAGTTCCAGAGCAAGACAGATCAAAAGACTG	1708
Db	332	EPROSERAPBARGIETHRARGPHEUHTRGUHPGELNMBLYSGIMILEYASHPTR	352
QY	1709	GAAGAAGCGCTTCATCGGCATCGGATGCGGACGATCAACCAAGCGCTGGTAGAGCT	1768
Db	352	PLYSLYBARGPHEIIEGLYILEARGMETARGHRIETHRPROSERLEUVALASPLUWE	372
QY	1769	GAAGGCCACGACCCCGAATTCCTCCAGAGGTCAGCAGTGAATTTATGTGCAAGAGTTGC	1828
Db	372	ULYSLASERASNPPOASPPHEPROGLIUALSERSERGLYIETRYVALGILGILVALAI	392
QY	1829	GCCGAATTCACCTTCTCGAGAGAGGGGAGCATCAAGATGSGTGCATCATGTCAGAGGTCA	1888
Db	392	APROMSERPROSEGLNARGLYGLYILEGINMBGLYASPLIEILEVALYVALAS	412
QY	1889	CGGCGCTCCTCTAGTGAATCTCAGTAGAGCTGCAGAGAGCGCTGTGACCGAGTCTCTCT	1944
Db	412	NGLYARGPROLEUVALASPSERSEGLUENGLNGLVALLEUTHGLUSERPROLE	432
QY	1949	CTTACTGAGAGGTGCGGCGGGGGAACGACGACTCTCTTCACAGCATGCACTGAGGTGCT	2008
Db	432	ULEULEUGILVALARGARGGLYASNAASPSAPLEUENPHESERILEALPROGLIUALVA	452
QY	2009	CATG 2012	
Db	452	Iwet 453	
RESULT 5			
US-10-381-820A-8			
: Sequence 8, Application US/10381820A			
: Publication No. US2004014233A1			
: GENERAL INFORMATION:			
: APPLICANT: Deshun, Lu			
: APPLICANT: Song, Ho Yeong			
: APPLICANT: Su, Eric Wen			
: APPLICANT: Wang, He			
: TITLE OF INVENTION: Novel Secreted Proteins and Their Uses			
: FILE REFERENCE: X-13974			
: CURRENT APPLICATION NUMBER: US/10/381,820A			
: CURRENT FILING DATE: 2003-03-27			
: NUMBER OF SEQ ID NOS: 8			
: SOFTWARE: PatentIn version 3.2			
: SEQ ID NO 8			
: LENGTH: 453			
: TYPE: PRT			
: ORGANISM: Homo sapiens			
US-10-381-820A-8			
Alignment Scores:			
Pctd. No.:		3,97e-97	Length: 453

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Qy	1829	GGCGAATTCACCTTCTTCAGAGAGCGGATCCAGATGATGTGACATTCATTCGCAAGTCCAA	1889
Db	392	apriamserProserglnatrgylgylieglnaspeiyaspllellevalyvalas	412
Qy	1889	CGGCGTCTCTTAATGTGACTCGATGTAGCTCAGAGAGCCGTGTGACCGAGTCTCTCT	1948
Db	412	nglyArgProleuvalnapsersergileuGlnGlnlvalvalleuthrgruserProle	432
Qy	1949	CTTACTGAGGTGCGGCGGCGAAACGACGACTCTCTTCAGCATTCGACCTTGAGTGTGT	2008
Db	432	uLeuGlnlvalArgargGlyAaanaAspLeuLeuPheSerilealProGluValva	452
Qy	2009	CATG 2012	
Db	452	Imet 453	
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; Sequence 14, Application US/11140224			
; Publication No. US2005027280A1			
; GENERAL INFORMATION:			
; APPLICANT: INCYTE GENOMICS, INC.			
; APPLICANT: DELEGANE, Angelo M.; LAL, Preeti G.			
; APPLICANT: HAPALIA, April U.A.; PATTERSON, Chandra			
; APPLICANT: WALIA, Natinder K.; KEARNER, Liam			
; APPLICANT: TRIBOULEY, Catherine M.; KHAN, Farrah A.			
; APPLICANT: YAO, Montique G.; BAUGHN, Mariah R.			
; APPLICANT: AZIMZAI, Yalda; ELLIOTT, Vicki S.			
; APPLICANT: NGUYEN, Damiel B.; GANDHI, Ameena R.			
; APPLICANT: YANG, Junning; HERNANDEZ, Roberto			
; APPLICANT: POLICKY, Jennifer L.; LU, Dyrung Anna M.			
; APPLICANT: REDDY, Roopa M.; YUE, Henry			
; APPLICANT: TANG, Y. Tom			
; TITLE OF INVENTION: PROTEASES			
; FILE REFERENCE: PI-0085 USN			
; CURRENT APPLICATION NUMBER: US/11/140,224			
; CURRENT FILING DATE: 2005-05-31			
; PRIOR APPLICATION NUMBER: US/10/275,505			
; PRIOR FILING DATE: 2002-11-04			
; PRIOR APPLICATION NUMBER: PCT/US01/14651			
; PRIOR FILING DATE: 2001-05-04			
; PRIOR APPLICATION NUMBER: 60/209,402			
; PRIOR FILING DATE: 2000-06-01			
; PRIOR APPLICATION NUMBER: 60/207,477			
; PRIOR FILING DATE: 2000-05-25			
; PRIOR APPLICATION NUMBER: 60/205,803			
; PRIOR FILING DATE: 2000-05-17			
; PRIOR APPLICATION NUMBER: 60/203,566			
; PRIOR FILING DATE: 2000-05-11			
; PRIOR APPLICATION NUMBER: 60/202,082			
; PRIOR FILING DATE: 2000-05-04			
; NUMBER OF SEQ ID NOS: 28			
; SOFTWARE: PERL Program			
; SEQ ID NO 14			
; LENGTH: 453			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc_feature			
; OTHER INFORMATION: incyte ID No: 7474343CD1			
US-11-140-224-14			
Alignment Scores:			
Pred. No.: 3,97e-97 Length: 453			
Score: 1668.00 Matches: 354			
Percent Similarity: 79.04 Conservative: 11			
Best Local Similarity: 76.64 Mismatches: 30			
Query Match: 29.94 Indels: 67			
DB: 6 Gaps: 7			
US-10-617-443B-1(1-3006) x US-11-140-224-14 (1-453)			

QY	749	GAGCTCCTCGCCAGCCCTGACAGAGGCTCCAGTGAAGGGGGGTGAGGAAGCCACGACATGCA	808
Db	19	GIuPPrOAlaAlaIPro-----CysPrOAlaArgCys	29
QY	809	AGCCCTTTTAAACCATTCCTCGGGGTGAGGAGCCCTTCC-----CAA	850
Db	30	AspAla-----SerArgCysProSerProArgCysProGlyGlyTyr	43
QY	851	ATGCTGTGTCATCTGCACTGCTGTGTGGTA-----GG	883
Db	44	ValProAspLeu-CysAsnCySylLeuValCysAlaAlaSerGluGlyIuProCysgl	63
QY	884	GGGTCCCCAAGGGGCTCAGTGTGGGCTAGAGCTG-----GCTCT	922
Db	63	YGIProLeuAspSerProCysGlyGluSerLeuLucyValArgGlyLeuCySerArgCy	83
QY	923	GAACTGGGAGCAGGGGTCTC-----	941
Db	83	SArgTTrpSerHisAlaValCysGlyThrAspGlyHisThrTyrAlaAsnValCysAlaLe	103
QY	942	-----AGGAAGAGCTCTCTCTCTCTGCCACTGGGCAATAGCCCTTGGGAGC	988
Db	103	UGlnAlaAlaSerArgAlaLeuGluLeuSerGlyThrProValArgGluLeuGluIu	123
QY	989	TGGCAGCATCGTGAATCTCATGATGACACTGGCCCTTCCCGCAGCGACAGTCTCCACA	104
Db	123	SGIYAlaLeuCysProLeu-----GlyLeuHisGI	132
QY	1049	GCTGAGCAGCCCGGCTCAAGTTCATCTTCTGTCGACGTGTGGAGAGAATCGCAC	110
Db	132	nLeuSerSerProArgTyrIuSPhAsnPhelIeAlaAspValValGluIuSleIeAlaPr	152
QY	1109	AGCCGTGTGCACATAGAGCTTCTTGAGACACCGCTGTTTGGCCGACGTCGCCCT	116
Db	152	AlaValValHisIleGluLeuPheLeuArgHisProLeuPheGlyArgAsnValProle	172
QY	1169	GTCCACGGGTCTGGCTTCATCATCTCAGAGCCGGCCCTGATCATCAACAATGCCACCT	122
Db	172	uSerSerIylSerGlyPheIleMetSerGluIuAGlyLeuIleIleThrAsnAlaHisVala	192
QY	1229	GGTGTCAGCAACAGTGTGTCGCCCGGAGGAGGACAGACTCAAGTGCACACTACAGATG	128
Db	192	IValSerSerAsnSerAlaAlaProGlyArgGluGluLeuIuSvalGluLeuGluAsnGI	212
QY	1289	GGACTCCTATGAGGCGCACATCAAGACATCGACAAAGAGTGGACATTGCCACCATCA	134
Db	212	YAspSerTyrGluAlaThrIleIuSAspIleAspIuSylSerAspIleAlaThrIleIu	232
QY	1349	GATCCATCCCAAGAAAAGCTCCCTGTGTGTGTGCTGGGTCACTGGCCGACCTGGGGCC	140
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Db	252	OGlyGluPheValValAlaIleIleGlySerProPheAlaLeuGluAsnThrValThrTrGI	272
QY	1469	CATGCTCAGCACTGGCCAGCGGAGGAGGAGGAGGAGCTGGGCTTCGGGACCTCGACATGGA	152
Db	272	YIleValSerThrAlaGluArgGluGlyArgGluLeuGluIuLeuArgAspSerAspMetAs	292
QY	1539	CTACATCCAGACGAGTGCATCATCACTACGGGAACTTCGGGGGACCACTGTGAACT	158
Db	292	PtyrIleGlnThrAspAlaIleIleAsnTyrGIYAsnSerGlyGlyProLeuValAsnIe	312
QY	1589	GGATGCGAGAGTCATTGGCATCAACAAGCTCAAGGTCAACGGTGGATTCCTTTGCCAT	164
Db	312	uAspGIuIuValIleIleGlyIleAsnThrLeuIuSValThrAlaGlyIleSerPheAlaI	332
QY	1649	CCCTTCACACCGCATCACAGGTTCTCTCAAGATGTCACAGAACAGCATCAAAAGCTG	170
Db	332	eProSerAspArgIleThrArgPheLeuThrGIuPheGluAspIuSValIleIuSAspTr	352
QY	1709	GAAGAAGCGCTTCATGGCATACGAGTGGAGCGATCACACCAAGCTGTGTGATAGCT	176

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Db 352 ptyblybAsgPheIleIlyleargMetAgtHrIleThProSerIeuValAspGluLe 372
1769 GAAGCCAGCAGCAGCCGAGCTCCAGAGGTCAGCAGTGAATTATGTGCAAGAGTTGC 1828
372 ulysAlaSerAsnProAspPheProGluValIserSerGlyIleTyxValGlnGluValAl 392
1829 GCGGATTCACCTTCTCAGAGAGCGGCGCATCCAAGATGGATCATCTCTCAAGGTCA 1888
392 aProAsnSerProSerIeuIlnArgIlyGlyIleGlnAspGlyAspIleIleValIySValAs 412
QY 1889 CGGCGCTCTCTAGTGAAGTCTGAGTGAAGTGAAGGCGGCTGTCGACCGAGTCTCTCT 1948
412 nGlyAArgProIeuValAspSerSerGluIeuGlnGluAlaValIeuThrGluSerProle 432
Db 432 ulleuGluValAlArgIlyAsnAspAspLeuIeuPheSerIleAlaProGluValVa 452
QY 2009 CATTG 2012
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Db 452 lmet 453
RESULT 8
US-09-796-753-34
; Sequence 34, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
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; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 34
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Mouse
US-09-796-753-34
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pred. No.:	2,99e-95	length:	348
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Percent Similarity:	97.1%	Conservative:	2
Best Local Similarity:	96.5%	Mismatches:	8
Query Match:	29.4%	Indels:	2
DB:	3	Gaps:	1

US-10-617-443b-1 (1-3006) x US-09-796-753-34 (1-348)

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Db 9 serGlyThrProValArgGlnIleuGlnIlysgIylAcysPro-----LeuGlyIeuHIs 26
QY 1047 CAGCTGAGCAGCCCGCGCTCAACAAGTTCAACTTATTCGAGCTGTGTGAGAAATCGCA 1106
Db 27 GlnIeuSerSerProArgIlyxPheAsnPheIleAlaAspValValGluIySleAla 46
QY 1107 CCAGCGGTGTGCACATAGAGCTTCTGAGACACCGGCTTTGGCCGCAAGTGCC 1166
Db 47 ProAlaValAlaHisIleGluIeuPheIeuAlaGlnIleuPheGlyArgAsnValPro 66
QY 1167 CTGTCCAGCGGTTGTGCTTTCATGTGACAGGCGCGCTGATCATCAACATGCCAC 1226
Db 67 IeuSerSerGlySerGlyPheIleIeuSerGlyAlaGlyIleuIleIleThraAsnAlaHis 86
QY 1227 GTGTGTCCAGCAACAGTGTGCTCCCGGCGAGCAGCCTCAAGTGTGACATGAGAT 1286
Db 87 ValIaSerSerAsnSerAlaAlaProGlyArgGlnIleuIySValGlnIeuGlnAsn 106
QY 1287 GGGGACTCTTATGAGGCGCAGCATCAAAAGATCGACAAGATCGAGACTGCCACATC 1346
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QY 1347 AAGATTCATCCCAAGAAAAAGCTCCGTGTGTGTGCTGAGTCACTCGGCGACCTGGCG 1406
Db 127 LysIleHisProIyIeuIySleuProValIleuIeuGlyHIsSerAlaAspIeuArg 146
QY 1407 CTTGGGAGATTGTGTGTGCGCATTCGCGACTCCCTTCGCGCTTACAAACACATGCAACG 1466
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QY 1467 GGCATCGTCAAGACTGCGCAGGCGAGGAGGAGGAGGAGTGGGCTCGGAGTCCGACATG 1526
Db 167 GlyIleValaSerThrAlaIleGlnArgGluGlyArgGluIleuArgAspSerAspMet 186
QY 1527 GACTACATCAAGCAGATGCCATCATCAACTACGAGAACTCCGGGAGACCATGTGTAAC 1586
Db 187 AspTyrlleGlnThrAspAlaIleIleIleAsnTyrgIyAsnSerGlyGlyProIeuValAsn 206
QY 1587 CTGATGCGAGGTGATTTGGCATCAACAGCTCAAGGTCAAGGCTGGCATCTCTTGGCC 1646
Db 207 LeuAspGlyGluValIleGlyIleAsnThrIleuIySValThrAlaGlyIleSerPheAla 226
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QY 1647 ATCCCTCAGACCGGATCAACAGGTTCTCAGAGATTCCAGAGATCAAGAC 1706
Db 227 ILeProserAspArgIleThrArgPheLeuThrGluPheGlnAspIleGlySer 246
QY 1707 TGGAGAGACGCTTCATCGGCATACGAGATGCGAGCATCAACAGCTGTGATGAG 1766
Db 247 TrpIleValSerPheIleGlyIleArgMetArgThrIleThrProSerLeuValAspGlu 266
QY 1767 CTGAAGGCGAGAACCCGAGACTCCAGAGGTGAGAGGAAATTATGCAAGGTT 1826
Db 267 LeuIleValSerAspProSerPheProGluValSerSerGlyIleThrValGlnGluVal 286
QY 1827 GCGCGCAATTCATCTTCAGAGAGCGGCATCAAGATGATGATCATCGTCAAGTCC 1886
Db 287 AlaProAsnSerProSerGlnArgIleGlyIleGlnAspGlyAspIleIleValIleVal 306
QY 1887 AACGGCGCTCTCTAGTGAAGCTGAGAGTGCAGAGAGCGGTGTGTCGAGTCTCT 1946
Db 307 AsnGlyArgProLeuValAspSerSerGluLeuGlnGluValIleLeuThrGluSerPro 326
QY 1947 CTCCTACTGAGAGGTGCGGCGGAGAACGAGCACTCTCTTCAGATGCGACCTGAGTGC 2006
Db 327 LeuLeuLeuGluValAlaArgArgIleAsnAspAspLeuLeuPheSerIleAlaProGluVal 346
QY 2007 GTCATG 2012
Db 347 ValMet 348
RESULT 9
US-10-485-313A-27
; Sequence 27, Application US/10485313A
; Publication No. US20050059002A1
; GENERAL INFORMATION:
; APPLICANT: NIE, Guiying
; APPLICANT: SALMONSEN, Lois Adrienne
; APPLICANT: LI, Ying
; APPLICANT: HAMPTON, Anne Lorraine
; APPLICANT: FINDLAY, John Kerr
; TITLE OF INVENTION: Novel Serine Protease
; FILE REFERENCE: 31633-200357
; CURRENT APPLICATION NUMBER: US/10/485, 313A
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: PCT/AU02/01010
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: PR6707
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-485-313A-27
Alignment Scores:
Pred. No.: 6,69e-90 Length: 459
Score: 1554.00 Matches: 329
Percent Similarity: 76.44 Conservative: 24
Best Local Similarity: 71.24 Mismatches: 42
Query Match: 27.94 Indels: 67
Gaps: 7
US-10-617-443B-1 (1-3006) x US-10-485-313A-27 (1-459)
QY 749 GAGCCTCTGCGCCAGCTAGAGGGGTTCAGTAGGGGGGTGAGAGAACCCAGACGTGGA 808
Db 25 GluProAlaAlaPro-----CysProAlaArgCys 35
QY 809 AGCCTTTTAACATTCCTCGGGGTGAGGAGCCCTTCC-----CAA 850
Db 36 AspAl-----SerArgCysProSerProArgCysProGlyGlyTyr 49
QY 851 ATGCTGTGTCTACTGACGTGCTGTGTGTA-----GG 883

Db 50 ValProAspLeu-CysAsnCysCysLeuValCysAlaAlaSerGluGlyGluProCysIle 69
QY 884 GGGTCCCAACCGGCTCAGTGTGGCTGAGGCTG-----GCTCT 922
Db 69 YArgProLeuAspSerProCysGlyAspSerLeuGluCysValArgGlyValCysArgCys 89
QY 923 GAACGTGGAGCGGGTCTC----- 941
Db 89 bArgTrpThrHisThrValCysGlyThrAspGlyHisThrTyrAlaAspValCysAlaLe 109
QY 942 -----AGAAAGAGCTCTCTCTCTCTCTGAGGATGAGGCTCTGAGAGC 988
Db 109 uGlnAlaAlaSerAlaGArgAlaLeuGlnValSerGlyThrProValArgGlnLeuGlnIly 129
QY 989 TGGCAGCATCGTATCTCATGATGACCTGAGCCCTTCCCGCAGCGCAGGTCTCCACCA 1048
Db 129 sGlyAla-----CysProSerGlyLeuHisIleG 138
QY 1049 GCTGAGCAGCGCGGCTCAAGTTCACTTCACTTGTGACCGTGGAGAGATGCGCNC 1108
Db 138 nLeuThrSerProArgTyrLysPheAsnPheIleAlaAspValValGluValIleAlaArg 158
QY 1109 AGCCGTGTCCACATAGAGCTCTTCTGAGACACCGGCTGTGGCCGCAAGTCCCT 1168
Db 158 cAlaValValHisIleGluLeuPheLeuArgHisProLeuPheGlyArgAsnValProle 178
QY 1169 GTCCAGCGGTTCTGCTTCATCATGTGACAGGCGGCTGATCATCACCAGTCCACGT 1228
Db 178 uSerSerGlySerGlyPheIleMetSerGlyAlaGlyLeuIleValThrAsnAlaHisVal 198
QY 1229 GGTGTCCAGCAAGTGTGCCCCGGGAGAGAGAGTCAAGGTGCAAGTGTCAAGATG 1288
Db 198 lValSerSerSerThrAlaSerGlyArgGlnIleuValGlnLeuGlnAsnI 218
QY 1289 GGACTCTATGAGGCGCACCATCAAAAGATGAGCAAGAGTGGCATTTGCCACATCA 1348
Db 218 yAspAlaTyrGluAlaThrIleGlnAspIleAspIleAspIleAlaThrIleVal 238
QY 1349 GATCCATCCCAAGAAAAGCTCCTGTGTGTGCTGGGTGATCCTGCGGCGACCTGCGGC 1408
Db 238 lIleHisProIlyLysIleuProValLeuLeuGlnIleHisSerAlaAspLeuArgPr 258
QY 1409 TGGGAGATTGTGGTGGCGCATCGGACCTCTTGCCTTACAGAACACAGTGAACAGCG 1468
Db 258 oGlyGlnPheValAlaIleGlySerProPheAlaLeuGlnAsnThrValThrThrX 278
QY 1469 CATGTCAGCACTGCCAGCGGAGGAGGAGGAGGCTCGGAGCTCCGACATGGA 1528
Db 278 yIleValSerThrAlaGlnArgAspGlyLysGluLeuGlyLeuArgAspSerAspMetCAs 298
QY 1529 CTACATCCAGACGATGCGATCATCACTACCGGAACTCCGGGGAGCACTGTGTAACCT 1588
Db 298 pTyrIleGlnThrAspAlaIleIleAsnTyGlyAsnSerGlyProLeuValAsnLe 318
QY 1589 GATGCGCAGGTGATGGCATCAACGCTCAAGGTCAAGCTGGCATCTCTTGGCAAT 1648
Db 318 uAspGlyGluValIleGlyIleAsnThrLeuLysValAlaIleGlyIleSerPheAlaI 338
QY 1649 CCCCTCAGACCGCATCAACAGGTTCTCTCAGAGATGTCAGAGACAGATCAAGACTG 1708
Db 338 eProSerAspArgIleThrArgPheLeuSerGluPheGlnAsnLysHisValIleAspTr 358
QY 1709 GAAGAAGCTTCATCGGCATACGATGCGGACGATCAACACAGCTGTGTGATGACT 1768
Db 358 pIleValSerPheIleGlyIleArgMetArgThrIleThrProSerLeuValGluGluLe 378
QY 1769 GAAGCGCAGCAACCCGATCTCCAGAGGTGACAGATGAGATTTATGCAAGAGGTGC 1828
Db 378 uLysAlaAlaAsnProAspPheProAlaValSerSerGlyIleTyrValGlnGluValVa 398
QY 1829 GCCGAATTCACCTTCTCAGAGAGCGGATCATCAAGATGTGATCATCATCGTCAAGGTCA 1888

Db 398 1ProabnserrProserGlnArgGlyGlyTlleglnAapRglaApeRllelleVallyeValAs 418
 QY 1889 CGGGCGCTCTTAGTGAGCTGAGTGAGCTGAGAGGCGCTGAGACCGAGTCTCTT 1948
 Db 418 nGlytrgProleuAlaAspserSerGluLeuGlnGlnAlaValLeuAaMgIusezSerle 438
 QY 1949 CCTACTGGAGGAGCGCGCGGGGAGACAGACCTCCCTCAGACCTGAGCTGAGTGT 2008
 Db 438 tleuLeuGlnValArgArgGlyAaMhAapRleuLeuPheSerllelleProGlnValVa 458
 QY 2009 CATG 2012
 Db 458 lmet 459
 RESULT 10
 US-10-301-822-79
 / Sequence 79, Application US/10301822
 / Publication No. US20030148410A1
 / GENERAL INFORMATION:
 / APPLICANT: Millennium Pharmaceuticals, Inc.
 / APPLICANT: Berger, Allison
 / APPLICANT: Guillemette, Tracy L.
 / APPLICANT: Kamatkar, Shubhangt
 / APPLICANT: Schlegel, Robert
 / APPLICANT: Monahan, John E.
 / APPLICANT: Thibodeau, Stephen N.
 / APPLICANT: Burger, Lawrence J.
 / TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
 / TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 / FILE REFERENCE: MPM01-0292RNM
 / CURRENT APPLICATION NUMBER: US/10/301,822
 / CURRENT FILING DATE: 2002-11-21
 / PRIOR APPLICATION NUMBER: US 60/339,971
 / PRIOR FILING DATE: 2001-12-10
 / PRIOR APPLICATION NUMBER: US 60/361,978
 / PRIOR FILING DATE: 2002-03-05
 / PRIOR APPLICATION NUMBER: US 60/381,988
 / PRIOR FILING DATE: 2002-05-20
 / NUMBER OF SEQ ID NOS: 228
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 79
 / LENGTH: 452
 / TYPE: PRT
 / ORGANISM: Homo Sapiens
 / US-10-301-822-79
 Alignment Scores:
 Pred. No.: 1,99e-89 Length: 452
 Score: 1546.50 Matches: 343
 Percent Similarity: 76.9% Conservative: 14
 Best Local Similarity: 73.9% Mismatches: 37
 Query Match: 27.7% Indels: 72
 DB: 4 Gaps: 8
 US-10-617-443b-1 (1-3006) x US-10-301-822-79 (1-452)
 QY 749 GAGCTCTCCGCCAGCTTACAGAGTCCAGTGAAGGGGGTGAGGAAGCCAGACGCTGA 808
 Db 19 GlnProProAlaAlaPro-----CysProAlaArgCys 29
 QY 809 AGCCTTTTAAACCATTTCTCGGGGTGAGCGAGCCCTTCC-----CAA 850
 Db 30 AspVal-----SerArgCysProSerProArgCysProGlyGlyTyr 43
 QY 851 ATGCTGTGTGCTCACTGACTGTGTGTGTA-----GG 883
 Db 44 ValProAspLeu-CysAaMhCysCysLeuValCysAlaAlaSerGlnGlyLupProCysG 63
 QY 884 GGGTCCCAACGGGCTCAGTGTGGGCTGAGGCTG-----GCTCT 922
 Db 63 yGlyProLeuAapSerProCysGlyLupSerLeuGlnCysValArgGlyLeuCysArgC 83

QY 923 GAATGGAGACAGGGCTCTC----- 941
 Db 83 sArgtrPheRhlAaValCysGlyThrAapRlyHlserHrYrAlaAaValCysAla 103
 QY 942 -----AGGAAGAGCTCTCTCTCTCTGAGCACTGGAGCACTAAGCCCTGGAGAC 988
 Db 103 uGlnAlaAlaSerArgAaValAlaLeuGlnLeuSerGlyThrProValArgGlnLeuGln 123
 QY 989 TGGAGACATCGTGTCACTGATGACCTGGACCTTCCCGCAGCGAGCTTCACCA 1048
 Db 123 sGlyAlaCysProLeu-----GlyLeuHlser 132
 QY 1049 GCTGAGACAGCCCGGCTCACTCAAGTTCATCTTCTGAGTGTGAGAGATGGCACC 1108
 Db 132 nLeuSerSerProArgTyrLysPheAaMhPheilleAlaAspValValGlnLyslleAla 152
 QY 1109 ACCGTGTCTCCATNAGACTTCTTCTGAGACACCCGCTGTTGGCCGAGAGTGGCCCT 1168
 Db 152 oAlaValAlaHlserlleGlnLeuPheLeuArgHlProLeuPheGlyArgAaValProle 172
 QY 1169 GTCCAGCGGTTCTGCTTCATCATGTGACAGGCGCGCTGATCATCACCAGTCCACGT 1228
 Db 172 userSerGlySerGlyPheilleMetSerGlnAlaGlyLeuIlelleThrAaMhHlserVa 192
 QY 1229 GGTGTCCAGCAACAGTGTGCTGCCCGGAGCGAGCACTCAAGGTGACCTCAAGATGG 1288
 Db 192 lValSerSerAaMhSerAlaAlaProGlyArgGlnGlnLeuLysValGlnLeuGlnAaMh 212
 QY 1289 GGATCTCTTAGAGCGCACCATGAAGACATGACAAAGTGGGACATTGGCCACCATCA 1348
 Db 212 yAspSerTyrGlnAlaThrIleLysAaMhLysAaMhLysAaMhLysAaMhLysAaMhL 232
 QY 1349 GATTCATCCCAAGAAAGAGCTCTGTTGTTGCTGAGTGTGCTGAGTGTGAGTGTGAG 1408
 Db 232 lIleHlserProLysLysLysLeuProValLeuLeuLeuGlnHlserAlaAspLeuArg-V 252
 QY 1409 TGGGAGATTGTGTGGCCATGAGGAGTCCCTTCCGCTCAAGAACACAGTACAAAGGG 1468
 Db 252 aGlySerLeuTyrLupProSer-GluSerLeuArgProThrGlnHlserAaMhGlnGly 271
 QY 1469 CATCGTCACACATGCCCGGAGGAGGAGGAGGAGTGGGCTCCGGAGATCCGACATGGA 1528
 Db 272 ---lleValAlaLeuProSerGlyGlnGlyAlaGlyProProGlyLeuArgHlserGly 290
 QY 1529 CTACATCC-AGACGAGTGCATCATC-AACTACGGGAAGTCCGGGAGACCATGTGTAAC 1586
 Db 291 leuHlserThrArgArgMetProSerSerAaMhTyrGlyAaMhSerGlyLysProLeuValAaMh 310
 QY 1587 CTGATGGCGAGGTCTTTGGCATCAACAGCTCAAGGTCAAGGCTGGCATCTCTTGGC 1646
 Db 311 leuAaMhGlyGlnValilleGlylleAaMhThrLeuLysValThrAlaGlylleSerPheAla 330
 QY 1647 ATCCCTCAGACCGCATCACAGGTTCTCTCAAGAGTTCCAAGACAGACAGATCAAGAC 1706
 Db 331 lIleProSerAaMhArgHlserThrArgPheLeuThrGlnPheGlnAaMhLysGlnleLysAaP 350
 QY 1707 TGGAGAGACGCTTCACTGCGCATACGATGCGGACATGACACCAAGCTGTGTGATGAG 1766
 Db 351 CysLysLysArgPheHlserlleGlylleArgMetArgThrIleThrProSerLeuValAaMh 370
 QY 1767 CTGAAGCCAGCAACCCGAGCTTCCAGAGGTCAAGAGTGAATTTATGTGCAAGAGGTT 1826
 Db 371 leuLysAlaSerAaMhProAaMhPheProGlnValSerSerGlylleTyrValGlnGlnVal 390
 QY 1827 GGGCGAATTCACCTTCTGAGAGGCGGATCCAGATGAGTGAATTCGTCAGAGTCT 1886
 Db 391 AlaProAaMhSerProSerGlnArgGlylleGlnAaMhLysAaMhLysAaMhLysAaMh 410
 QY 1887 AACGGCGTCTCTTAGTGAATTCGAGTGAAGCTGACAGAGGCGGTGCTGACAGAGTCTCT 1946
 Db 411 AaMhGlyArgProLeuValAaMhSerSerGlnLeuGlnGlnValAlaValLeuThrGlnSerPro 430
 QY 1947 CTCTTACTGAGGTGCGGCGGAGAAAGACGACCTCTCTTCAAGCATCGACCTGAGGTG 2006

DB 431 LeuLeuLeuGluValArgArgGlyAsnAspAspLeuLeuPheSerIleAlaProGluVal 450
QY 2007 GTCATG 2012
DB 451 ValMet 452

RESULT 11
US-09-764-898-256
; Sequence 256, Application US/09764898
; Patent No. US20020090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0201
; CURRENT APPLICATION NUMBER: US/09/764,898
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 256
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (32)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (35)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (42)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (104)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-898-256

Alignment Scores:
Pred. No.: 8,61e-79 Length: 286
Score: 1378.00 Matches: 275
Percent Similarity: 98.6% Conservative: 0
Best Local Similarity: 98.6% Mismatches: 4
Query Match: 24.7% Indels: 0
DB: 3 Gaps: 0

US-10-617-443B-1 (1-3006) x US-09-764-898-256 (1-286)

QY 1176 GGTTCGTGCTTATCATGTCAGAGGCGGCTGATCATACCAATGCCAGCTGTGTC 1235
DB 8 GlySerGlyPheIleuSerGluAlaGlyLeuIleIleThrAsnAlaIleValValSer 27

QY 1236 AGCAACAGTGTGCTGCGGCGGAGAGAGTCAAGTGCAGTCAAGTGCAGTGCAGTGC 1295
DB 28 SerAsnSerAla***ProGly***GlnGlnLeuLysValGln***GlnAsnLysAspSer 47

QY 1236 TATGAGGCGCACCATCAAGACATCGACAAAGAGTGGACATTCACCATCAAGATCAT 1355
DB 48 TyrGluAlaThrIleLysAspIleAspLysLysSerAspIleAlaIleThrIleLysIleHis 67

QY 1356 CCCAAGAAAAGCTCCCTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1415
DB 68 ProLysLysLysLeuProValLeuLeuLeuGlyHisSerAlaAspLeuArgProGlyGlu 87

QY 1416 TTTGTGTGGCATCGGAGTCCCTTGCCTTACAGAAACAGTGCAGACGGGATCGTC 1475
DB 88 PheValValAlaIleGlySerProPheAlaLeuGlnAsnThrValThr***GlyIleVal 107

QY 1476 AGCACTGCCAGCGGAGGAGGAGAGTGCAGTGCCTCCGAGACTCCGACATGACATCATC 1535
DB 108 SerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAspSerAspMetAspTyrIle 127

QY 1536 CAGACGATGTCATCATCACTACGAGAACTCCGGGGAGACCACTGTGAACCTGGATGAC 1595
DB 128 GlnThrAspAlaIleIleAsnIleIleAsnIleIleAsnIleIleAsnIleIleAsnIle 147

QY 1596 GAGTCATTTGCGATCAACAGCTCAAGGTCAAGGTCAAGGTCAAGGTCAAGGTCAAG 1655
DB 148 GluValIleGlyIleAsnThrLeuValThrAlaGlyIleSerPheAlaIleProSer 167

QY 1656 GACCGCATCAACAGGTCTCTCAACAGATTCACAGACAGCATGAAGTCAAGTCAAG 1715
DB 168 AspArgIleThrArgPheLeuThrGluPheGlnAspLysGlnIleLysAspTyrLys 187

QY 1716 CGCTTCATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGG 1775
DB 188 ArgPheIleGlyIleAsnMetArgThrIleThrProSerLeuValAspGluLeuVal 207

QY 1776 AGCAACCGGACTTCCAGAGGTCAAGGTCAAGGTCAAGGTCAAGGTCAAGGTCAAG 1835
DB 208 SerAsnProAspPheProGluValSerSerGlyIleTyrValGlnGluValAlaProAsn 227

QY 1836 TCACCTTTCAAGAGGCGGATCCAGATGTGATCATCATCTGCAAGTCAACGGGCT 1895
DB 228 SerProSerGlnArgGlyGlyIleGlnAspGlyAspIleIleValLysValAsnGlyArg 247

QY 1896 CCTTATGAGCATCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1955
DB 248 ProLeuValAspSerSerGluLeuGlnAlaValLeuThrGluSerProLeuLeu 267

QY 1956 GAGTGTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2012
DB 268 GluValArgArgGlyAsnAspAspLeuLeuPheSerIleAlaProGluValValMet 286

RESULT 12
US-10-485-313A-34
; Sequence 34, Application US/10485313A
; Publication No. US2005005902A1
; GENERAL INFORMATION:
; APPLICANT: NIE, Guiying
; APPLICANT: SALMONSEN, Lois Adrienne
; APPLICANT: LI, Ying
; APPLICANT: HAMPTON, Anne Lorraine
; APPLICANT: FINDLAY, John Kerr
; TITLE OF INVENTION: Novel Serine Protease
; FILE REFERENCE: 31633-200357
; CURRENT APPLICATION NUMBER: US/10/485,313A
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: PCT/AU02/01010
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: PR6707
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-313A-34

Alignment Scores:
Pred. No.: 2,54e-64 Length: 357
Score: 1150.00 Matches: 251
Percent Similarity: 73.0% Conservative: 11
Best Local Similarity: 69.9% Mismatches: 30
Query Match: 20.6% Indels: 67
DB: 5 Gaps: 7

US-10-617-443B-1 (1-3006) x US-10-485-313A-34 (1-357)

QY 749 GAGCTCTCTGCTCCAGCTTCAGAGGTCCAGTGAAGGGGGGTAGAGAACCCAGACGTGA 808
DB 19 GluProProAlaAlaPro-----CysProAlaArgCys 29

QY 809 AGCTTTTAACCATTTCTGCGGGGTAGAGAGCCCTTCC-----CAA 850

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Db      30 AspVal-----serArgCysProSerProArgCysProGlyGlyTyr 43
      851 ATGCGTGTGTACTGCACTGCTGTGTGTA-----GG 883
      44 ValProAspLeu-CysAsnCysCysLeuValCysAlaAsnSerGlyGlyProCysGly 63
      884 GGGTCCCAACGGGCTCAGTGTGGCTGAGGCTG-----GCTCT 922
      63 yGlyProLeuAspSerProCysGlyGlySerLeuGlyCysValArgGlyLeuCysArgCys 83
      923 GAATGGGACAGGGGTCTC----- 941
      83 sArgTPrSerHisAlaValCysGlyThrAspGlyHisThrTyrAlaAsnValCysAlaLe 103
      942 -----AGGAAGAGCTCTCTGCTGCCCACTGGGCAATGAGCTCTGGAGAC 988
      103 uGlnAlaAlaSerThrArgAlaLeuGlnLeuSerGlyThrProValArgGlnLeuGlnLys 123
      989 TGGCAGCATGTGATCTCACTGATGACCTGGCCCTCCCGCAGGCAAGTCTCCACCA 1048
      123 sGlyAlaCysProLeu-----GlyLeuHisGly 132
      1049 GCTGAGCAAGCCCGGCTACAAAGTCAATTGCTGACGTGTGGAGAAAGATCCACCC 1108
      132 nLeuSerSerProArgTyrLysPheAsnPheIleAlaAspValValGlyLysIleAlaPr 152
      1109 AGCGGTGTGCATAGACTCTTCTGAGACACCCCGCTGTTGGCCGCAAGTGCCTCT 1168
      152 cAlaValValHisIleGlyLeuPheLeuArgHisProLeuPheGlyTyrAsnValProle 172
      1169 GTCCAGCGGTTCTGGCTCATCATGTCAAGAGCCGCGCTGATCATCAACAAATGCCACGT 1228
      172 uSerSerGlySerGlyPheIleMetSerGlyAlaGlyLeuIleIleThrAsnAlaHisVa 192
      1229 GGTGTCCAGCAACAGTGTGCTGCTGCGGAGGAGGAGAGTCAAGGTGCAAGATGG 1288
      192 ValSerSerAsnSerAlaAlaProGlyArgGlnGlnLeuLysValGlnLeuGlnAsnGly 212
      1289 GAATCTCTTGAAGCCACCATCAAGACATCGAAGAAAGTCCGACATTTGCCACCATCAA 1348
      212 yAspSerTyrGlnAlaThrIleLeuAspIleAspLysSerAspIleAlaThrIleLys 232
      1349 GATTCATCCCAAGAAAGCTCCCTGTGTGTTGCTGGGTGCACTGGCGGCACTGGCGGC 1408
      232 sIleHisProLysLysLeuProValLeuLeuLeuGlyHisSerAlaAspLeuArgPr 252
      1409 TGGGAGTTTGTGGTGGCCATCGGAGTCCCTTCGCTTACAGAAACAAGTACAAAGGG 1468
      252 oGlyGluPheValValAlaIleGlySerProPheAlaLeuGlnAsnThrValThrThrGly 272
      1469 CATGTGACAGCTGCCAGCGGAGGAGGAGGAGGAGGAGCTCCCGGAGCTCCGACATGGA 1528
      272 yIleValSerThrAlaGlnArgGlnGlyArgGlnLeuGlyLeuArgAspSerHisPheHis 292
      1529 CTACATTCACAACGGAATGCACTCATCACTACGGGAACTCCGCGGAGCACTGTGTGAACCT 1588
      292 pTyrIleGlnThrAspAlaIleIleLeuTyrGlyAsnSerGlyGlyProLeuValAsnLe 312
      1589 GAATGGGAGGCTTGTGATCAACACGCTCAAGGTCAAGCTCGGATCTCTTGGCAT 1648
      312 uAspGlyGlyValIleGlyIleAsnThrLeuLysValThrAlaGlyIleSerPheAlaIle 332
      1649 CCCCTCAGACCGCATCAGCGTTCCACAGAGTTCCAAAGATTCAAAGCAAGCATCAA 1703
      332 eProSerAspArgIleThrArgPheLeuThrGluPheGlnAspArgIleLys 350

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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P3201
CURRENT APPLICATION NUMBER: US/09/764,898
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 311
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 184
LENGTH: 330
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (244)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (265)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-898-184

Alignment Scores:
Pred. No.: 1,72e-62 Length: 330
Score: 1121.00 Matches: 241
Percent Similarity: 75.5% Conservative: 8
Best Local Similarity: 73.0% Mismatches: 32
Query Match: 20.1% Indels: 49
Gaps: 3
DB:

US-10-617-443b-1 (1-3006) x US-09-764-898-184 (1-330)
      791 GGAAGCCCAAGACGTCGAGAGCTTTTAACCATTCGAGGAGTGAAGCCCTTCCCA 850
      18 GlySerProGly-LeuGlnGlnPheGlyThrSerAlaSerGlnGlyPro----- 34
      851 ATGCTGTGTCACTGACTGCTGTGTGAGGGGTGTCCTCCCAAGGCTCAGTGTGGGCT 910
      35 -----CysGlyGlyProLeuAspSerProCysGlyGly 45
      911 GAGGCTG-----GCTCTGAACCTGGACAGGGGTCTC----- 941
      45 uSerLeuGlyCysValArgGlyLeuCysArgCysArgTPrSerHisAlaValCysGlyThr 65
      942 -----AGGAAGACCTTCT 955
      65 rAspGlyHisThrTyrAlaAsnValCysAlaLeuGlnAlaAsnArgAlaLeuGly 85
      956 CTTCTGCGCCACTGGGCAATGAGCTCTGAGAGCTGAGCAATCGATCTCACTGATGCA 1015
      85 nLeuSerGlyThrProValArgGlnLeuGlnLysGlyAlaCysProLeu----- 101
      1016 CTGGGCCCTTCCCGCAGGCGCAGGTCTCCACAGCTGAGACAGCCCGCTCAAGTTCAA 1075
      102 -----GlyLeuHisGlnLeuSerSerProArgTyrLysPheHis 114
      1076 CTTGATTTGACAGTGTGTGAGAAAGATCCACAGCGGTGTCACATAGACTCTTCT 1135
      114 nPheIleAlaAspValValGlnLysIleAlaProAlaValIleHisIleGluLeuPheLe 134
      1136 GAGACACCGCTGTTGGCCGCAACGTGCCCTGTCCAGCGGTTCTGCTTCATCATGTGC 1195
      134 uArgHisProLeuPheIleThrAsnAlaHisValIleSerSerHisSerHisAlaProGly 174
      1196 AGAGCGGCGCTGATCATCAACATGCCCACTGAGGTGTCAGAGCAAGAGTGTGCCCGGG 1255
      154 rGluAlaGlyLeuIleIleThrAsnAlaHisValIleSerSerHisSerHisAlaProGly 174
      1256 CAGGAGAGGCTCAAGGTGACGTACAGAAATGGGACTCTTATGAGGCCACCATCAAGA 1315
      174 yArgGlnGlnLeuLysValGlnLeuGlnAsnGlyAspSerTyrGlnAlaThrIleLysAs 194
      1316 CATTCACAAGAGTGTGACATTTGCCACCATCAAGATTCATCCCAAGAAAGATCCCTGT 1375
      194 pIleAspLysLysSerAspIleAlaThrIleLysIleHisProLysLysLeuProVa 214

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RESULT 13
 US-09-764-898-184
 ; Sequence 184 Application US/09764898
 ; Patent No. US20020090673A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.

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QY 1376 GTTGTGCTGGGTCACTCGGCGGAGCTTGGGAGTTGTGCTGCGCATCGGCG 1435
DB 214 lIeuLeuLeuGlyHsSerAlaAspLeuArgProGlyGluPheValAlaIleGlySe 234
QY 1436 TCCCTTCGCGCTTACAGAAACACAGTGAACAAGGAGCATCTGCACACTGCGGAGG 1495
DB 234 rProheAlaLeuGlnAsnThrValThr**GlyIleValSerThrAlaGlnArgGlu 254
QY 1496 CAGGAGCTGGGCTTCGCGGAGCTCGGAGCATGAGCTACATCCAGACGAGATGCATCA 1555
DB 254 YArgGluLeuGlyLeuArgAspSerAspMet**TyrIleGlnThrAspAlaIleIleAs 274
QY 1556 CTAACGGAATCCCGGCGGAGCACTGTTGAACCTGATGGCGAGTCAATGGCATCAAC 1615
DB 274 nTyrGlyAsnSerGlyGlyProLeuValAsnLeuAspGlyGluValIleGlyIleAsnTh 294
QY 1616 GCTCAAGCTCAGCGGTGATCTCTTTCGCTCCATCCCTCAGACCGCATCAGCGTTCT 1675
DB 294 rLeuValThrAlaGlyIleSerPheAlaIleProSerAspArgIleThrArgPhele 314
QY 1676 CACAGAGTTCCAAGACACAGCATCAA 1703
DB 314 uThrGluPheGlnAspLysGlnIleLys 323

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RESULT 14

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US-10-485-313A-39
/ Sequence 39, Application US/10485313A
/ Publication No. US20050059002A1
/ GENERAL INFORMATION:
/ APPLICANT: NTE, Guiying
/ APPLICANT: SALAMONSEN, Lois Adrienne
/ APPLICANT: Li, Ying
/ APPLICANT: HAMPTON, Anne Lorraine
/ APPLICANT: FINDLAY, John Kerr
/ TITLE OF INVENTION: Novel Serine Protease
/ FILE REFERENCE: 31633-200357
/ CURRENT APPLICATION NUMBER: US/10/485, 313A
/ PRIOR FILING DATE: 2004-01-30
/ PRIOR APPLICATION NUMBER: PCT/AU02/01010
/ PRIOR FILING DATE: 2002-07-30
/ PRIOR APPLICATION NUMBER: PR6707
/ NUMBER OF SEQ ID NOS: 55
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 39
/ LENGTH: 363
/ TYPE: PRF
/ ORGANISM: Mus musculus
US-10-485-313A-39

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Alignment Scores:

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Pred. No.: 1,45e-59 Length: 363
Score: 1075.00 Matches: 234
Percent Similarity: 71.3% Conservative: 22
Best Local Similarity: 65.2% Mismatches: 36
Query Match: 19.3% Indels: 67
DB: 5 Gaps: 7

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US-10-617-443b-1 (1-3006) x US-10-485-313A-39 (1-363)

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QY 809 AGCCTTTTAAACATCTCGGGGTGAGCGAGCCCTTTC-----CAA 850
DB 36 AspVal-----SerArgCysProSerProArgCysProGlyGlyTyr 49
QY 851 ATGCGTGGTGCATGCTGCTGTGTGTA-----GG 883
DB 50 ValProAspLeu-CysAsnCySerLeuValCysAlaIleSerGluGlyGluProCysG 69

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QY 884 GGGTCCCAAGCGGCTCAGTGGGCTGAGGCTG-----GCTCT 922
DB 69 YArgProLeuAspSerProCysGlyAspSerLeuGluCysValArgGlyValCysArgCys 89
QY 923 GAATGGGACAGGGGTCTC----- 941
DB 89 sArgTrpThrIleThrValCysGlyThrAspGlyHisThrTyrAlaAspValCysAlaIle 109
QY 942 -----AGGAAGAGCTCTCTCTCTGCGCACTGGGAGCATAGGCTTGGGAGC 988
DB 109 uGlnAlaAlaSerAlaArgAlaLeuGlnValSerGlyThrProValArgGlnLeuGlnIly 129
QY 989 TGGCAGCATCTGATCTCAGTATGACCTGAGCCCTTCCCGGACGAGCATGCTCCACCA 1048
DB 129 sGlyAla-----CysProSerGlyLeuHisG 138
QY 1049 GCTGAGACCCCGCTACAGTTCAACTTCAATTGCTGACGCTGTGGAGAGAGATGCAAC 1108
DB 138 nLeuThrSerProArgTyrLysPheAsnPheIleAlaAspValValGluValIleAlaPr 158
QY 1109 AGCGGTGCTCCATAGAGCTCTTCTGAGACACCCGCTGTTGGCCGCAAGTCCCT 1168
DB 158 oAlaValAlaHisIleGluLeuPheLeuArgHisProLeuPheGlyArgAsnValProle 178
QY 1169 GTCCAGCGGTTCTGCTCATCATGTCAAGAGCGGCTGATCATCACCAATGCCACGT 1228
DB 178 uSerSerGlySerGlyPheIleMetSerGlnAlaGlyLeuIleValThrAsnAlaHisVal 198
QY 1229 GGTGTCAGCAACAGTGTGCTCCCGGAGGAGGAGCATGAGTCAAGTCAAGATG 1288
DB 198 lValSerSerSerSerThrAlaSerGlyArgGlnGlnLeuLysValGlnLeuGlnAsnG 218
QY 1289 GAGCTCTTATGAGGCGCACCATTAAGACATGACACAAAGTGGACATTTGCCACCATCA 1348
DB 218 YAspAlaTyrGluAlaThrIleGlnAspIleAspLysSerAspIleAlaThrIleVal 238
QY 1349 GATCATCCCAAGAAAGAGCTCTGTTGTGCTGGGCTCACTGCGGAGCCTCGGCG 1408
DB 238 lIleHisProLysLysLysLeuProValLeuLeuLeuGlyHisSerAlaAspLeuArgPr 258
QY 1409 TGGGAGGTTTGTGTCATCGGAGTCCCTTGCCTTACAGAAACAGTGAACGCG 1468
DB 258 oGlyGluPheValValAlaIleGlySerProheAlaLeuGlnAsnThrValThrTrG 278
QY 1469 CATGTCAGCACTGCCAGCGGAGGAGGAGGAGCTGGGCTTCGCGAGCTCCGACATGGA 1528
DB 278 YIleValSerThrAlaGlnArgAspGlyLysGluLeuGlyLeuArgAspSerAspMetAs 298
QY 1529 CTACATCCAGAGATGTCATCATCACTACGGAAGTCCGGGGGAGCCACTGGTGAACCT 1588
DB 298 pTyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyProLeuValAsnLe 318
QY 1589 GGATGGCGAGGTGATTTGATGATCAACACGCTCAAGGTCAAGGCTGCGATCTCTTGGCAT 1648
DB 318 uAspGlyGluValIleGlyIleAsnThrLeuLysValAlaAlaGlyIleSerPheAlaIle 338
QY 1649 CCCCTCAAGCCGATCAACAGGTTCTCTCAAGAGTCTCCAAAGACACAGATCAA 1703
DB 338 eProSerAspArgIleThrArgPheLeuSerGluPheGlnAsnLysHisValLys 356

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RESULT 15

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US-10-170-385-355
/ Sequence 355, Application US/10170385
/ Publication No. US20030203372A1
/ GENERAL INFORMATION:
/ APPLICANT: Ward, Neil Raymond
/ APPLICANT: Mundy, Christopher Robert
/ APPLICANT: Kan, On
/ APPLICANT: Harris, Robert Alan
/ APPLICANT: White, Jonathan
/ APPLICANT: Binley, Katie Mary
/ APPLICANT: Rayner, William Nigel
/ APPLICANT: Naylor, Stuart

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/ APPLICANT: Kingsman, Susan Mary
 / APPLICANT: Krige, David
 / TITLE OF INVENTION: ANALYSIS METHOD
 / FILE REFERENCE: 53268200100
 / CURRENT APPLICATION NUMBER: US/10/170,385
 / CURRENT FILING DATE: 2002-06-12
 / PRIOR APPLICATION NUMBER: PCT/GB02/01662
 / PRIOR FILING DATE: 2002-04-08
 / PRIOR APPLICATION NUMBER: PCT/GB01/05458
 / PRIOR FILING DATE: 2001-12-10
 / NUMBER OF SEQ ID NOS: 549
 / SOFTWARE: PatSeq for Windows Version 4.0
 / SEQ ID NO 355
 / LENGTH: 480
 / TYPE: PR1
 / ORGANISM: Homo Sapiens
 / US-10-170-385-355

Alignment Scores:
 Pred. No.: 1,27e-58 Length: 480
 Score: 1060.50 Matches: 241
 Percent Similarity: 63.5% Conservative: 69
 Best Local Similarity: 49.4% Mismatches: 117
 Query Match: 19.0% Indels: 61
 Gaps: 12

US-10-617-443b-1 (1-3006) x US-10-170-385-355 (1-480)

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 Db 48 ProInProglunHsCyvsglglYlAtrgAlaTrgAp----- 60
 QY 618 AGAGGGCAGATTCTCTCTGTAGGGGTATTGCTGTAGCATGAGGAAACAGACAGGCCCA 617
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 Db 61 -----AlaCys-----GlyCysgsluValCysglYalAProglunYalA 74
 QY 678 GGG---GGACTRACCCGATCCAGACCCCGGCTCAGTCCGCTGAGGCTCAGGCAATAT 724
 Db |||||
 Db 75 AlaCysglYleuInglnGlYProCysglYgluYleuInglnCys----- 89
 QY 735 CCTAACCTCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGGAA 794
 Db -----ValValPro-----PheglYalProAlaSerAlaThrVal 101
 QY 795 GCCCAGCAGTGAAGCCTTTTAAACATCTCGGGGGTGAAGCGGCGCTCCCAATATG 854
 Db ::::|
 Db 102 AtrgAtrgAlaGlAlaGlYleuCyvAlCysAlaSerSerGlYProVal----- 118
 QY 855 CTGGTCTCACTGACCTGCTGTGTGTAGGGGGTCCCAACGGGCTCAGTGTGGGCTGAG 914
 Db |||||
 Db 119 -----CysglYSerAerAlaAenThrYrAlaAenLeuCyglInleuAtrg 133
 QY 915 CTGGCTGTGAATGGAGCAGGGGCTCAGAAAGCTCTCTCTGCTCCCACTGGGAT 974
 Db |||||
 Db 134 AlaAla-----SerAtrgSerSerGlYalrYleu-----His 143
 QY 975 AGGCTCTGGAGCTGGACAGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 1034
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 Db 144 AtrgPro-----ProValIleValLeuInglnYalA-----CysglY 156
 QY 1035 GCAGCTCTCCACAGCTGAGCAGCCCGCTCAAGTTCATCTTCTGAGCAGCTGAGCTG 1094
 Db |||||
 Db 157 GlnglYglnGlunHrProAenSerleuAtrgHleuYrYlAenPheIleAlaAerValVal 176
 QY 1095 GAGAAGATGGCAGCCGCTGGTCCATGAGCTCTCTGAGCAGCCCGCTGAGCTGAGCTG 1154
 Db |||||
 Db 177 GlulYleuAlaProAlaValAlaHisIleGlulYleuPheAtrgYleuProPheSerYs 196
 QY 1155 CGCAAGCTGGCCCTGTCTCAGCGCTTCTGCTTCACTGTCAGAGCGCGGCTGATCATC 1214
 Db |||||
 Db 197 ArgGlulValProValAlaSerSerGlYPheIleValSerSerGlunSerGlulYleuVal 216
 QY 1215 ACCAATGCCACGTGTGTCTCAGACACAGTGTGCGCGGCGAGGCGAGCTCAAGCTG 1274

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 Db 217 ThrAenAlaHisValAlaThrAen-----LysHisAtrgValYalVal 230
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 Db 231 GlulYleuAenGlYalAtrgYrYlAenYsIleYsAerValAerGlulYsAlaAer 250
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 Db 251 IleAlaLeuIleYsIleAerPheIleGlnGlYleuPheProValLeuLeuLeuGlYalrYleu 270
 QY 1395 GCCGACCTGGCGCTGGAGATTGT 1454
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 Db 271 SerIleuAtrgProglYgluPheValAlaIleGlySerProPheSerleuInglnAen 290
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 Db 291 ThrValThrTrgYrYleValSerThrThrGlnAtrgGlYglYleuInglnYleuAtrg 310
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 Db 311 AenSerAerPheAerYrYleGlnThrAerAlaIleAenYrYlAenSerleuYglY 330
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 Db 351 IleSerPheAlaIleProSerAerPheYsIleYsYsPheLeuThrGlulSerHisAerAtrg 370
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 Db 371 GlulAlaYsGlYlYalAlleThrYleuYsYrYlGlyIleAtrgMetSerleu 390
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 Db 411 GlYalAtrYrIleIleGlulValIleProAerPheProAlaGlulAglYlYleuYsGl 430
 QY 1866 GGTGACATCATGCTCAAGCTCAACGGGCTCTCTAGTGAAGCTCAGTGAAGCTGAGGAG 1925
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 Db 431 AenAerValIleIleSerIleAenGlYlnSerValIleSerAlaAenAerValSerAer 450
 QY 1926 GCGGTGCTGACCGAGTCTCTCTCTTACTGAGAGTGGCGGCGGAGCAAGACCTCCCTC 1985
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 Db |||||
 Db 471 IleThrValIleProglunIle 478

Search completed: February 21, 2006, 21:01:50
 Job time : 443 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: February 21, 2006, 20:48:06 ; Search time 4.1 Seconds
(without alignments)
2068.023 Million cell updates/sec

Title: US-10-617-443B-1

Perfect score: 5578
Sequence: 1 cagggactcgaagcttgcag.....gccaaaaaataaaaaaaa 3006

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 108093 segs, 14239677 residues

Total number of hits satisfying chosen parameters: 216186

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

MODEL=frame_n2p.model -DEV=xlp
-O=/abs/ABSSWB/spool/US10617443/runat_21022006_165450_15843/app_query.fasta.1
-DB=Published Applications AA New -QPMF=faetan -SUFFIX=n2p.rapbn -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptco -NORM=ext -HEAPSIZE=500 -MILEN=0
-MAXLEN=200000000 -HOST=abs802p
-USER=US10617443@cgn1_1_7 -runat_21022006_165450_15843 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications AA New.*

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5: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1546.5	27.7	452	7	US-11-186-284-79 Sequence 79, Appl
2	1060.5	19.0	480	6	US-10-821-234-1465 Sequence 1465, Ap
3	1043.5	18.7	447	7	US-11-072-512-2765 Sequence 2765, Ap
4	903.5	16.2	458	7	US-11-183-914-11 Sequence 11, Appl
5	535	9.6	109	7	US-11-053-076-59 Sequence 59, Appl
6	496	8.9	100	7	US-11-107-096-78 Sequence 78, Appl
7	425	7.6	474	7	US-11-098-686-10591 Sequence 10591, A
8	424.5	7.6	499	6	US-10-467-657-2096 Sequence 2096, Appl
9	387	6.9	441	6	US-10-454-437-56 Sequence 56, Appl

10	335.5	6.0	423	7	US-11-074-176-4 Sequence 4, Appl1
11	318	5.7	317	6	US-10-793-626-1824 Sequence 1824, Ap
12	309.5	5.5	1717	7	US-11-182-016-20 Sequence 20, Appl
13	309	5.5	1466	7	US-11-186-284-33 Sequence 33, Appl
14	293.5	5.3	1166	6	US-10-821-234-964 Sequence 964, Appl
15	277.5	5.0	1742	7	US-11-182-016-23 Sequence 23, Appl
16	266.5	4.8	1717	7	US-11-182-016-20 Sequence 20, Appl
17	262	4.7	1733	7	US-11-182-016-21 Sequence 21, Appl
18	260.5	4.7	493	6	US-10-793-626-1832 Sequence 1832, Ap
19	259.5	4.7	115	6	US-10-485-788A-774 Sequence 774, App
20	259.5	4.7	115	6	US-11-053-076-152 Sequence 152, App
21	254.5	4.6	1496	7	US-11-186-284-35 Sequence 35, Appl
22	251.5	4.5	1733	7	US-11-182-016-21 Sequence 21, Appl
23	248	4.4	1464	7	US-11-186-284-28 Sequence 28, Appl
24	248	4.4	1464	7	US-11-021-603-2 Sequence 2, Appl1
25	248	4.4	1467	6	US-10-821-234-1096 Sequence 1096, Ap
26	247	4.4	1464	7	US-11-000-463-243 Sequence 243, App
27	245.5	4.4	1377	6	US-10-821-234-1070 Sequence 1070, Ap
28	245	4.4	1823	6	US-10-995-561-988 Sequence 988, App
29	245	4.4	2102	6	US-10-995-561-990 Sequence 990, App
30	245	4.4	2157	6	US-10-995-561-991 Sequence 991, App
31	243.5	4.4	1464	7	US-11-000-463-243 Sequence 243, App
32	243.5	4.4	1464	7	US-11-186-284-28 Sequence 28, Appl
33	243.5	4.4	1464	7	US-11-021-603-2 Sequence 2, Appl1
34	243.5	4.4	1467	6	US-10-821-234-1096 Sequence 1096, Ap
35	242	4.3	2108	6	US-10-995-561-989 Sequence 989, App
36	239	4.3	101	7	US-11-107-096-77 Sequence 77, Appl
37	235.5	4.2	1730	7	US-11-182-016-19 Sequence 19, Appl
38	233.5	4.2	1874	6	US-10-821-234-1182 Sequence 1182, Ap
39	233	4.2	1767	6	US-10-995-561-911 Sequence 911, App
40	233	4.2	1767	6	US-10-995-561-914 Sequence 914, App
41	233	4.2	1806	6	US-10-995-561-912 Sequence 912, App
42	233	4.2	1806	6	US-10-995-561-915 Sequence 915, App
43	233	4.2	1818	6	US-10-995-561-910 Sequence 910, App
44	233	4.2	1818	6	US-10-995-561-913 Sequence 913, App
45	231.5	4.2	1742	7	US-11-182-016-23 Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-11-186-284-79
; Sequence 79, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kametkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John B.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MP001-029P2RM
; CURRENT APPLICATION NUMBER: US/11/186,284
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 452
; TYPE: PR
; ORGANISM: Homo Sapiens


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Db      75 AlaCysGlyLeuGlnGluGlyProCysGlyGluGlyLeuGlnCys----- 89
Qy      735 CCTAAGCTCTCTAGAGCTCTGAGCCAGCCAGCTCAGCGAGGCTCAGAGGGGGGTGAGAA 794
Db      90 -----ValValPro-----PheGlyValProAlaSerAlaThrVal 101
Qy      795 GCCCAGCAGCTGGAAGCCTTTTAAACATCTCGGGGTGAGCGAGCGCCCTCCCAATGC 854
Db      102 ArgAlaGAlaGlnAlaGlyLeuGlyValCysAlaSerSerGluProAla----- 118
Qy      855 CTGGTGTCACTGCACTGCTGTGTGTGTAGGGGGTCCCAACGGAGCTCAGTGTGGCTGAG 914
Db      119 -----CysGlySerAlaAlaThrValAlaAlaLeuGlySerGlnLeuArg 133
Qy      915 CTGGCTGTGAAGTGGGACAGAGGGGTCTCAGGAAGAGCTCTCTCTGCGCCACTGGGCT 974
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Qy      975 AGGCTCTGGAGAGTGGCAGCATCTGATCTCATGATGCACTGGCCCTTCCCGCAGC 1034
Db      144 ArgPro-----ProValIleValLeuGlnArgGlyAla-----CysGly 156
Qy      1035 GCAGGTCTTCACAGCTGAGCAGCCGCGCTACAGTTCACTTCACTTGTGAGTGTG 1094
Db      157 GlnGlnGlnGlnArgProAlaSerLeuArgHisGlyValAlaAlaAlaAlaVal 176
Qy      1095 GAGGAAGATGGCAGCAGCCCTGGTCCACATAGAGCTTCTTCTAGAGACCCCGCTTTGGC 1154
Db      177 GlnValIleAlaProAlaValAlaHisGlnLeuPheArgLeuValLeuProPheSerIlys 196
Qy      1155 CGCAAGCTGCGCCCTGTCAGCGAGTTCTGAGCTTCATGATCAGAGGCGCGCTGATCATC 1214
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Qy      1215 ACCAATGCCACGTGTGTTCAGCAAGAGTGTCTGCCCGGAGCGAGCAGCTCAAGTGTG 1274
Db      217 ThrAlaAlaHisIleValIleThrAla-----LysHisArgValIleVal 230
Qy      1275 CAGCTACAGATGGGAGCTCCATAGAGCGCCATCAAGATCAAGATCAAGAGTGGAGC 1334
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Qy      1335 ATTGGCACCATCAAGATCCATCCCAAGAAAGAGCTCCCTGTGTGTGTGTGGTCACTG 1394
Db      251 IleAlaLeuIleLysIleAlaPheIleGlnGlyLysLeuProValLeuLeuLeuGlyArgSer 270
Qy      1395 GCCGAGCTTGGCGCTTGGAGAGTTGTGTGTGCGCATGCGAGTCCCTTCGCGCTCAAGAA 1454
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Qy      1515 GACTCCGACATGAGATCAATCCAGAGAGATGCGATCAATCAATCAAGGAAATCCGGGGGA 1574
Db      311 AsnSerAspMetCAspArgTyrIleGlnThrAlaAlaIleIleAsnTyrGlyAsnSerGlyGly 330
Qy      1575 CCAGTGTGAACCTGGATGGAGAGGTGATGTGAGATCAACAGCTCAAGGTCAAGCTGGC 1634
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Qy      1635 ATCTCTTTGGCATCCCTCCAGACCGCATCAACAGGTCTCTCAAGAGTTCCAAAGCAAG 1694
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Qy      1746 AACCAAGCTCTGTGATGAGTGAAGAGCCAGCAACCGGATTTCCAGAGTCAAGCAT 1805
Db      391 ThrSerSerLysAlaLysLeuLysLysAspArgHisAspAspPheProAlaIleSer 410
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Qy      1866 GGTGACATCATGCTCAAGGTCAAGCGGCTCTCTAGTGAAGTCAAGTCAAGTCAAGAG 1925
Db      431 AsnAspValIleIleSerIleAsnGlyGlnSerValIleSerAlaAsnAspValIleSerAsp 450
Qy      1926 GCCGTGTGACCGAGATCTCTCTCTCACTGAGAGTGGCGGGGGAACGACACCTCTTC 1985
Db      451 ValIleLysArgGlnSerThrLeuAsnMetValValAlaArgArgGlyAsnGlnAspIleMet 470
Qy      1986 TTCAGATGCGACATGAGGTGGTC 2009
Db      471 IleThrValIleProGlnLeuIle 478

RESULT 3
US-11-072-512-2765
; Sequence 2765, Application US/11072512
; Publication No. US20060029945A1
GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHITO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARA, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2765
; LENGTH: 447
; TYPE: PRN
; ORGANISM: Homo sapiens
US-11-072-512-2765

Alignment Scores:
Pred. No.: 5,84e-56
Score: 1043.50
Percent Similarity: 65.1%
Best Local Similarity: 50.1%
Query Match: 18.7%
DB: 7
Gaps: 14

US-10-617-443B-1 (1-3006) x US-11-072-512-2765 (1-447)
609 CCATGAGAGAGGAGCCAGTTCTCTCC-----TGTAAG----- 641

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Db 22 ProArgHArgSerProAlaLeuAlaLeuSerAenThrTyrAlaAenLeuCyseGln 41
QY 642 -----GATATGCTGTAGCATGAGGAAAGAAAGAGCCCGAGGAGTAAACCGGAT 695
Db 42 ArgAlaGlyValAlaLeuArgGlyValAlaArgAlaArgGlyValArgValArg--- 60
QY 696 CCAAGCCCGGCTCTACTCCGCTGTGGCTCAAGCAATATCTTAACCTCTCTGTAGAGCTC 755
Db 61 ProAlaGlyValProValArgArgGlyValA-----AlaVal 72
QY 756 CTGCCCCAGCTTACAGAGGCTCAAGTGAAGGAGGAGTGAAGCCGACGCTGGAAGCCCTT 815
Db 73 ArgGlyValaLeuArgGlyAlaSerLeuGlyHileGlyAlaAlaAlaArg----- 88
QY 816 TTAAACATTCTCGGGGAGAGAGAGCCCTTCCAAATGCTCGTGTACTGCACTGCTGT 875
Db 89 -----AlaGlyArgProLeu-----Cys 94
QY 876 GTGGTAGAGGGATCCCAAGGAGCTCAAGTGTGGCTGAGGCTGCTGAACTGGAGAG 935
Db 95 Val-----ArgGlnGln-----LeuArgAlaAla----- 102
QY 936 GGTCTCAAGAAAGCCCTCTCTCTCTGCTCAAGGAGTGAAGCTTGGAGCTGGAGC 995
Db 103 ---SerArgArgSerGluArgLeu-----HisArgPro----- 112
QY 996 ATCGTATCTCATGATGACACTGGCCCTTCCGCGCAAGCCGAGCTTCCACAGCTGAGC 1055
Db 113 ProValAlaValaLeuGlnArgGlyAla-----CyseGlyGlnGlnGlnArgProAen 130
QY 1056 AGCCCGGCTTCAAGATTCAATTCTGCTGAGCTGTGTGAAGATGCAAGCCGCTG 1115
Db 131 SerLeuArgHileGlyTyrAenPheAlaAlaSerValAlaGlnLeuAlaAlaProAlaVal 150
QY 1116 GTCCACATTAAGCTCTTCTGAGACAGCCGCTGTGGCGCAAGCTGCTGCTGACG 1175
Db 151 ValHileGlyLeuPheArgGlyLeuPheArgGlyLeuPheSerGlyValProValAlaAlaSer 170
QY 1176 GGTTCGTGCTTCAATGATGACAGAGCCGCTGATCATCAATGCGGAGCTGCTGCTC 1235
Db 171 GlySerGlyPheAlaAlaSerGlnArgGlyLeuAlaAlaThrAlaAlaValAlaThr 190
QY 1236 AGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1295
Db 191 Aen-----LysHisArgValValLeuValGlnLeuLysAenGlyAlaThr 204
QY 1296 TATGAGGCCCATCAAAAGCATGACAGAAAGTGGACATTCGACCATCAAGATTCAT 1355
Db 205 TyrGlnAlaLysIleLysAspValAspGlnLysAlaAlaAlaAlaLysIleAsp 224
QY 1356 CCCAAGAAAAGCTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1415
Db 225 HisGlnGlyLysLeuProValaLeuLeuLeuGlyArgSerSerGlnLeuArgProGlyGln 244
QY 1416 TTTGTGTGTGTCATCGGAGCTCTTGTGCTTACAGAAACAGTGAACAGGAGCTGCTC 1475
Db 245 PheValValaAlaAlaGlySerProPheSerLeuGlnAenThrValaThrThrGlyLeVal 264
QY 1476 AGCAGTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1535
Db 265 SerThrThrGlnArgGlyGlyLysGlnLeuGlyLeuArgAenSerAspMetAspTyrIle 284
QY 1536 CAGACGGATGTCATCATCACTACGGAATCTCGGGGAGACATGTGTGAACGTGATGAGC 1595
Db 285 GlnThrAspAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 304
QY 1596 GAGGTATTGGCATCAACAGCTCAAGTCAAGCTGAGCTGCTGCTGCTGCTGCTGCTGCT 1655
Db 305 GluValaIleGlyIleAenThrLeuLysValaThrAlaGlyIleSerPheAlaAlaProSer 324
QY 1656 GACCGGATCAACAGGTTCTCAAGAGTTCCAAAGATTCAAAGC----- 1706
Db 325 AspLysIleLeuLysPheLeuThrGlnSerHisAspArgGlnAlaLysGlyLysAlaIle 344

QY 1707 TGGAAAGACGCTTCAATCGGCATACGATCGGAGCATCAACCAAGCTGCTGATGAG 1766
Db 345 ThrLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 364
QY 1767 CTGAAGGACGACCAACCCGAGCTTCCAGAGTCTGAGCAGTGAATTAATGTCMAAGGTT 1826
Db 365 LeuLysAspArgHileArgAspPheProAspValIleSerGlyAlaTyrIleIleGlnVal 384
QY 1827 GCGCCGAATTCACCTTCTCAAGAGGCGGAGCTCAAGATGTGATCATCTGCAAGGTC 1886
Db 385 IleProAspThrProAlaGlnAlaGlyGlyLeuLysGlnAenAspValIleIleSerIle 404
QY 1887 AACGGGCTCTCTAGTGAATCTGAGTACGTGACAGAGCCGCTGACCAAGTCTCT 1946
Db 405 AenGlyGlnSerValaValSerAlaAenAspValaSerAspValaLysArgGlnSerThr 424
QY 1947 CTCTTCAAGAGTGTGCGGCGGAGAAAGACAGACTCTCTTCAAGATCGCACTGAGGTG 2006
Db 425 LeuAenMetValaValaArgArgGlyAenGlnAenPheIleMetIleThrValaIleProGlnGln 444
QY 2007 GTC 2009
Db 445 Ile 445
RESULT 4
US-11-183-914-11
? Sequence 11, Application US/11183914
? Publication No. US20050282214A1
? GENERAL INFORMATION:
? APPLICANT: Bandman, Olga
? APPLICANT: Hillman, Jennifer L.
? APPLICANT: Yue, Henry
? APPLICANT: Guebler, Karl J.
? APPLICANT: Corley, Neil C.
? APPLICANT: Tang, Tom Y.
? APPLICANT: Shah, Purvi
? TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
? NUMBER OF SEQUENCES: 24
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Incyte Pharmaceuticals, Inc.
? STREET: 3174 Porter Dr.
? CITY: Palo Alto
? STATE: CA
? COUNTRY: USA
? ZIP: 94304
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FastSeq for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/11/183,914
? FILING DATE: 19-JULY-2005
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/09/008,271
? FILING DATE: 16-Jan-1998
? ATTORNEY/AGENT INFORMATION:
? FILING DATE: <Unknown>
? NAME: Mohan-Peterson, Sheela
? REGISTRATION NUMBER: 41,201
? REFERENCE/DOCKET NUMBER: PF-0458 US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650-855-0555
? TELEFAX: 650-845-4166
? INFORMATION FOR SEQ ID NO: 11:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 458 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear

;
; IMMEDIATE SOURCE:
; LIBRARY: SINIUCT01
; CLONE: 2680548
US-11-183-914-11

Alignment Scores:

Pred. No.:	1,528-47	Length:	25
Score:	903.50	Matches:	42
Percent Similarity:	65.18	Conservative:	9
Best Local Similarity:	45.38	Mismatches:	11
Query Match:	16.28	Indels:	44
DB:	7	Gaps:	12

US-10-617-443B-1 (1-3006) x US-11-183-914-11 (1-458)

QY	680	GGGACTAACCCGGAGTTCAGCCCGGGCTCACTCCCGTGTGGCTCAGCGCATATCTCTAA	733
Db	26	GlyAlaArgProAlaGlyLeuThrProAspLeuAlaLeu--LeuThrSer-----	41
QY	740	CCTCTCTGTAGACCTCTGCCAGCGCTAGCAGGGTTCAGTGAAGGGGGGTGAAGACCA	799
Db	42	GlyThrSerAspProAlaArgAlaArgAlaThrTy-----GlyThrPro	55
QY	800	GCACGTGAGACCTTTTAAACCATTCCTGGGGGTGACGAGCCCTTCCAAATGCTGTGT	859
Db	56	Ser-LeuThrAlaArgLeuSerVal--GlyAlaThrGluPro--ArgAlaCysLeuThr	73
QY	860	GTCACGTGACGTGTGTGTGTAGGGGGGCC---CAACGGGGTCACTGTGGGCTTAGAGCT	916
Db	73	rSer-----GlyThrProGlyProAlaGlnLeu-----Th	84
QY	917	GGCTCTGAACCTGGACAGGGGTCTCAGGAAGAGCTCTCTCTCCGCCACTGCGGCAATAG	976
Db	84	AlaValAlaThrProAspThrArgThrAlaGluAlaSerGluAsnSerGlyThrArgSerzAr	104
QY	977	G-----CCTCTGGAGCTGGCAGCATCGTATCTCACTGATG-----	1011
Db	104	GAlaAlaTrpLeuAlaValAlaLeuGlyAlaGlyAlaValLeuLeuLeuLeuTrpGlyGly	124
QY	1014	-----CACCTGGCCCTTCCGCCAGCGCAGGTCTCCACACAGCTGAGCAGGCGCGG	1066
Db	124	YGIAlaArgGlyProProAlaValAlaLeuAlaAlaAlaProSerProProAlaSerProAr	144
QY	1064	CTACAAGTTCACATTCATTTGCTGACGTGGTGGAGAAAGATTCGACACGCGGTGTCACAT	1122
Db	144	GSerGlnTrpAsnProIleIleAlaAspValValGluTrpThrAlaProAlaValAlaTrpTrl	164
QY	1124	AGAGCTCTTTCCTGAGACACCGGCTGTTGGCCGCAACGTGCCCTGTCCAGCGGTTCTGG	1188
Db	164	eglIuLeuAspArgHisProPheLeuGlyArgGluValProIleSerAsnGlySerGly	184
QY	1184	CTTATCATGTGCAGAGGCGCGGTATATATCAACCAATGCGCCAGTGGTGTCCAGACAG	1244
Db	184	yPheAlaValAlaAlaAspGlyLeuIleAlaThrAsnAlaHisValAlaAlaAsp----	202
QY	1244	TGCTGCCCCGGGCGAGCAGCTCAAGGTGCAGCTACAGAAATGGGAGCTCCTATGAGGC	1302
Db	203	-----ArgArgArgValArgValArgLeuAsnSerGlyAspThrTyGluAl	218
QY	1304	CACCATCAAAGACATGCACAGAGAGTGGACATTGGCACCATCAAGATCATCCACAGA	1366
Db	218	avalAlaThrAlaValaAspProValAlaAspIleAlaThrLeuArgIleGlnThrLysGly	238
QY	1364	AAAGCTCCCTGTGGTGTGGTGGGTGCACCTCGGCGCAGCGCGGCGGGAGATTTGTGT	1422
Db	238	uProLeuProThrLeuProLeuGlyArgSerAlaAspValAlaGlnGlyGluPheValaVala	258
QY	1424	GGCATTCCGGACAGTCCCTTCCGCTTACAGAAACAAGTGAACAAGGGGATGTCCAGACTGC	1483
Db	258	AlaMetGlySerProPheAlaLeuGlnAsnThrIleThrSerGlyIleValSerSerAl	278
QY	1484	CCAGCGGAGGGCAGGAGCTGGGCTCCGGGACTCCGACATGAGACTACATCCAGACGGA	1544

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Db      278 aglnargPrCoAlaArgspReuNglyLeuProGlnInThrAsnValGluIuYrIleGlnInThrAs 298
Qy      1544 TGCCATCATCTACTACCGGAACTCCGGGGGACCACTGGTGAACCTGGATGGCGAGGTCAT 1603
Db      298 pAlaAlaIleAspPheUlnHisArgIleGlyLysIleProLeuValAsnLeuAspGlyGluVal11 318
Qy      1604 TGGCATCAACACGGTCAAGGTCACGGGTGGCATCTCTTGGCCATGCCCTTCAGACGGCAT 1663
Db      318 eGlyValAsnThrMetCysValInrAlaGlyIleSerPheAlaIleProSerAspArgLe 338
Qy      1664 CACACGGTCTCTCCACAGAGTTCACAGAACAGCAG-----ATCAAGAAGCTGGA 1711
Db      338 uArgGluPheLeuHisArgIleGlyLysIleYasnSerSerSerGlyIleSerGlySerG1 358
Qy      1712 GAGCGCTTCAATCGGCATACCGATCGGACGATGACACCAAGCCTGGTGATGAGCTGMA 1771
Db      358 nArgArgTyrIleGlyValMetMetLeuThrLeuSerProSerIleLeuAlaGluLeuG1 378
Qy      1772 GCGCAGCAACCCGGAAGCTCCACAGGTCACACAGTGAATTTATGTGACAGAGGTTGGCC 1831
Db      378 nLeuArgGluProSerPheProAspValGlnHisGlyValLeuIleHisIlyValIleLe 398
Qy      1832 GAATTCACCTTCTCAGACAGCGCGGCATCAAGATGTGATCATCTGCATGCTCAACCG 1891
Db      398 uGlySerProAlaHisArgAlaGlyLeuArgProGlyAspValIleLeuAlaIleGlyG1 418
Qy      1892 GCGTCTCTAGATGAGCTCGAGTGAAGCTGACAGAGAGCCGTGCTGACCGATGTCCTTCT 1951
Db      418 uGlnMetValGlnAsnIaGluAspValTyrGluAlaValaLarghrGlnSerGlnLeuA1 438
Qy      1952 ACTGGAGTGGCGGGGGGGAACAGACGACCTTCCTTGAAGATGCCACTGAGNG 2006
Db      438 aValGlnIleArgTArgIArgGlyArgGluThrLeuThrLeuTyrValThrProGluVal 456

RESULT 5
US-11-053-076-59
; Sequence 59, Application US/11053076
; Publication No. US20050255460A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Somoza Diaz-Sarmiento, Chamorro
; APPLICANT: Belmares, Michael P.
; TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
; FILE REFERENCE: VITA-008CIP
; CURRENT APPLICATION NUMBER: US/11/053,076
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: PCT/US03/28508
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/409,298
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 109
; TYPE: PRT
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: ORGANISM: Homo sapiens	
US-11-053-076-59	
Alignment Scores:	
Pred. No.:	1,94e-25
Score:	535.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	9.6%
DB:	7
US-10-617-443B-1 (1-3006) x US-11-053-076-59 (1-109)	
QY	1674 CTCAAGAGATTCCAGACAGAGATCAAGACTGGAAGCGCTTCATCGCATACG 1733
DB	1 Leuhtngluphngclnsplysoinllelyabprrplylsyapghelleilylearg 20
QY	1734 ATGGGAGCATACACCAAGCCTGTGTGATGAGCTGAAGCCAGCAACCCGACTTCCA 1733
DB	21 MetargtnrllethrProserleuValaspJuleuylsAlaserAmProasphepro 40
QY	1794 GAGCTCAGACAGTGAATTTATATGCAAGAGTGTGGCCGAATTCCCTTTCAGAGAGC 1833
DB	41 GluValSerSeGlyIletryValInglnuValaProasSerProserGlnargly 60
QY	1854 GGCAATCAAGAGTGTGACATCATCGTCAAGGTCAACGGGCGCTCTAGTGAATCGAGT 1913
DB	61 GlyIleGlnaspGlyAspIlelleVallybValaenglyAargProleuValaspSer 80
QY	1914 GAGCTCAGAGAGCCGTGTGACCGAGTCTCTCTTCTTACGTGAGGTGCGGCGGCAAC 1973
DB	81 GlueuGnglnuValValleuThrGlnSerProleuLeuGlnuValArgGlyAsn 100
QY	1974 GACGACTCTCTTCCTCAGC 1991
DB	101 AspaSpLeuLeuPheSer 106
RESULT 6	
US-11-107-096-78	
: Sequence 78, Application US/11107096	
: Publication No. US20060003348A1	
: GENERAL INFORMATION:	
: APPLICANT: SIDHU, SACHDEV S.	
: APPLICANT: ZHANG, YINGNAN	
: TITLE OF INVENTION: OMI PDZ MODULATORS	
: FILE REFERENCE: P2100R1	
: CURRENT APPLICATION NUMBER: US/11/107,096	
: CURRENT FILING DATE: 2005-04-15	
: PRIOR APPLICATION NUMBER: US 60/563,157	
: PRIOR FILING DATE: 2004-04-16	
: NUMBER OF SEQ ID NOS: 79	
: SEQ ID NO 78	
: LENGTH: 100	
: TYPE: PRT	
: ORGANISM: Homo sapiens	
US-11-107-096-78	
Alignment Scores:	
Pred. No.:	4.27e-23
Score:	496.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	8.9%
DB:	7
US-10-617-443B-1 (1-3006) x US-11-107-096-78 (1-100)	
QY	1713 AAGCGCTTCATCGGATCGAGTGGAGCGATCAACCAAGCCTGGTGAAGCTGAAG 1772
DB	1 LysatgPheIleGlyIleargMechargtnrllethrProserleuValaspJuleuys 20
QY	1773 GCCAGCAACCCGACTTCCAGAGTCAAGCTGAAGTGAATTTATGTGCAAGAGTTGCCCG 1832

Db	21	AlaSerAanPProAbpPheProGluValSerSerGlyIleTyrValGlnGluValAlaPro	40
Qy	1833	AATTCACCTTCTCAGAGAGCGCGCATCCAGATGGTGAATCATCATGTCACAGGCGG	1892
Db	41	AanSerProSerGlnArgGlyGlyIleGlnAapGlyAapIleIleValIleValAanGly	60
Qy	1893	CGTCTCAAGAGACTCGAGTGAAGTGGAGAGCGCGCTGACCGAGTCCCTCTCTCTA	1952
Db	61	ArgProLeuValAapSerSerGluLeuGlnGluValLeuTrnGluSerProLeuLeu	80
Qy	1953	CTGGAGGTGCGCGCGGGAGACGACGACCTCTCTTCAGCATCGACCTGAGGTGATCATG	2012
Db	81	LeuGluValArgArgGlyAanAaAapPheLeuPheSerIleAlaProGluValValMet	100
RESULT 7			
US-11-098-686-10591			
/ Sequence 10591, Application US/11098686			
/ Publication No. US20060024696a1			
/ GENERAL INFORMATION:			
/ APPLICANT: Kapur, Vivek and Gebhart, Connie J.			
/ TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES			
/ TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING			
/ FILE REFERENCE: 09531-128001			
/ CURRENT APPLICATION NUMBER: US/11/098, 686			
/ CURRENT FILING DATE: 2005-04-04			
/ PRIOR APPLICATION NUMBER: PCT/US03/31318			
/ PRIOR FILING DATE: 2003-10-01			
/ PRIOR APPLICATION NUMBER: US 60/416,335			
/ PRIOR FILING DATE: 2002-10-04			
/ NUMBER OF SEQ ID NOS: 11433			
/ SOFTWARE: FastSeq for Windows Version 4.0			
/ SEQ ID NO 10591			
/ LENGTH: 474			
/ TYPE: PRT			
/ ORGANISM: Lawsonia intracellularis			
US-11-098-686-10591			
Alignment Scores:			
Pred. No.: 8,71e-19 Length: 474			
Score: 425.00 Matches: 138			
Percent Similarity: 45.9% Conservative: 83			
Best Local Similarity: 28.6% Mismatches: 173			
Query Match: 7.6% Indels: 88			
DB: 7 Gaps: 17			
US-10-617-443B-1 (1-306) x US-11-098-686-10591 (1-474)			
Qy	978	CCTCTGGAGAGTGGCAGAGATGTAATCTCACTGATGCACTGGCCCTTCCCGCAGCGCA	1037
Db	21	ProThrIleAlaGluSerAlaLeuProAanPheValIleProLeuValIyAaPAlaSerLys	40
Qy	1038	GGTCTCCACGACGTCGAGCAGC-----CCGCGCTACAAGTTCACCTTCATTGCT	1085
Db	41	AlaValValAanIleSerThrGlnLysLysIleProArgGlyArgThrGlnPhePromet	60
Qy	1086	GACCTGTGGAGAAAGATCGACACCGCGGTGTCACATAGAGCTTTCCTG-----	1136
Db	61	GluMetPheArgGlyLeuProProGlyI-----PheGluArgPhePheGluGlnPhe	77
Qy	1137	-----AGACACCGCGTGTGGCGCGACGTCGCCCTGTCCAGCGGTTCTGCTTCATC	1190
Db	78	GluProLysGlyProAaPbSerGlnIleHisLysGlnArgSerLeuGlyThrGlyPheIle	97
Qy	1191	ATGTCAAGAGCGCGCTGATCATCATCAACAAATGCCACAGTGTGTTCACAAACATGCTGCC	1250
Db	98	IleSerSerAapGlyTyrIleValThrAanAanHisValIleGlu-----	112
Qy	1251	CCGGGAGGACGACGACGCTCAAGGTGCACCTACAG-----AATGGGAGACTCTAT	1298
Db	113	---GlyAlaAapSerValArgValAanLeuGlnLysIleThrSerGlyLysGluGluSerLeu	131
Qy	1299	GAGCGACCATCAAAAGACATCGACCAAGAGTTCGACATTGCCACCATCAAGATTCATCCC	1358

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Db      132  ProAlaGluValIleGlyArgAspGluGluThrAspLeuAlaLeuLeuValLysSer 151
Qy      1359  AAGAAAAGCTCCCTGTGTGTTGCTGGGTCACTGGCGGAGCTGGCGGCTGGAGTTT 1418
Db      152  LysAspSerLeuProTyrLeuIlePheGlyAsnSerAspThrMetCylValIleGluTyr 171
Qy      1419  GTGGTGGCGGAGGAGCTCCCTGCGCTACAGAAAGATGACAGGAGGAGCTGGCAGC 1478
Db      172  ValLeuAlaIleGlyAsnProPheGlyLeuGlyHisThrValThrAlaGlyIleLeuSer 191
Qy      1479  ACTGCCAGCGGAGGAGGAGGAGCTGGGCTCCGGAGCTCCGACATGAGTACATCCAG 1538
Db      192  Ala-----LysGlyArgAspIleHisAlaGlyProPheAsp---AsnPheLeuGln 207
Qy      1539  ACGGATGCCATCATCACTACAGGAACTCCGGGGAGCCACTGTGTAACCTGGATGGCAG 1598
Db      208  ThrAspAlaSerIleAsnProGlyAsnSerGlyGlyProLeuIleAsnMetSerGlyGln 227
Qy      1599  GTGATTGGCATCAACGCTCAAGGTCACAGGCT-----GGCATGCTCTTGGCATCCCC 1652
Db      228  ValValGlyIleAsnThrAlaIleMetAlaSerGlyGlnGlyIleGlyPheAlaIlePro 247
Qy      1653  TCAGACCGCATCACAGGTTCTCTCACAGAGTTCCAAAGACAGACAGATCAAGATCGAAG 1712
Db      248  SerSerMetAlaAspArgIleIleGluGlnLeu-----LysThrAsnLysValSer 265
Qy      1713  AAGCCTTCATCGCATACGATCGGAGGAGATCACACCAAGCTGTGGATGAGCTGAAG 1772
Db      266  ArgGlyTyrPileGlyValThrIleGlnAspValAspThrAsnThrAlaLysAlaLeuGly 285
Qy      1773  GCCCAACACCGGAGCTCCAGAGGTGACAGAGTGAATTATGATGCAAGAGGTGGCGG 1832
Db      286  LeuSerGln-----AlaLysGlyAlaLeuValGlySerValValPro 299
Qy      1833  AATTCACTTCTCAGAGAGCGGATCCAAAGTGTGATCATCATCGTCAAGCTCAACGGG 1892
Db      300  GlyAspProAlaAspIleGlyValIleLeuLysValGlyAspIleValThrGlnAlaAspGly 319
Qy      1893  CGTCTCTAAGTGAAGTCCAGTGAAGTGCAGAGGCGGTCTGACGAGCTCTCTCTCA 1952
Db      320  LysGlnIleAspSerIleSerLeuLeuLysAlaIleAlaThrLysProPro----- 337
Qy      1953  CTGAGAGTGGCGGCGGAGAACAGACGACCTCTTCAGACATGCGACCTGAGGTGGTCAAG 2012
Db      338  -----PheSerValValLysLeuLysValTyr 346
Qy      2013  TGAGAGGCGCATCTCTCCAGCGCCAGACGCTCAGAGCTGACAGACAGGAGGCGAGCGCC 2072
Db      347  -----ArgAspGlyLysSerLysAspIleSerIleThrLeuGlyGlnArg 361
Qy      2073  CCCCCGAGATCAGACGAAGACACCGTGGTCTCTCAGCAGGCGGCGAGCTCTCTCTG 2132
Db      362  LysThrThrSerSerGlnLysGlnSerSerProGlnSerLeuProGlyAlaLeuGlyLeu 381
Qy      2133  GCTGTCGGGCGGAGAGCG-----GAGGCTGGGCTTGGCCAGGGG 2171
Db      382  SerValArgProLeuThrGlnGlnGlnLysSerPheAspValLysLeuGlyIleGly 401
Qy      2172  -----CCGAATTTCCGCTGGGAGTGTGATTCACATCCCG 2210
Db      402  LeuLeuValValSerValGluProAsnLysProAlaSerGluAlaGlyIle----- 418
Qy      2211  GTGCGCGGAGGAGGAGCCCAACATCCCTTGAACAGATATCTGAAAGTCACTTCCAG 2270
Db      419  -----ArgGlnGln-----AspIleIleLeu----- 425
Qy      2271  TTCTCGGATATTTCACAAAGTCCCTTCATGAGAGTCCCTCTCTCTAGCTTCCCGC 2330
Db      426  -----SerAlaAsnLeuLysProLeuGlnSerAlaAspAspLeuAlaAsnIle 441
Qy      2331  CTCTGC 2336
Db      442  IleCys 443

```

```

RESULT 8
US-10-467-657-2096
/ Sequence 2096, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SPA
/ APPLICANT: PONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASNIGNANI Vega
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ PRIOR FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqMan99, version 1.04
/ SEQ ID NO 2096
/ LENGTH: 499
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2096

Alignment Scores:
Pred. No.: 9,378-19 Length: 499
Score: 424.50 Matches: 135
Percent Similarity: 46.6% Conservative: 63
Best Local Similarity: 31.8% Mismatches: 137
Query Match: 7.6% Indels: 90
DB: Gaps: 14

US-10-617-443b-1 (1-3006) x US-10-467-657-2096 (1-499)
Qy      1083  GCTGACGTGGTGAGAGATGCGACACCGGTGTCAATAGACTTTCCTGAGA--- 1139
Db      58  AlaGlnLeuValGlnSerGlnGlyProAlaValAlaIleGlnAlaAlaProAlaPro 77
Qy      1139  ----- 1139
Db      78  ArgThrGlnAsnGlySerGlyAsnAlaGluThrAspSerAspProLeuAlaAspSerAsp 97
Qy      1140  -----CACCGCGCTTTGGCGCGCAAGTGGCC--- 1166
Db      98  ProPheTyrGluPhePheLysArgLeuValProAsnMetProGlnIleProGlnGlnGln 117
Qy      1167  -----CTGTCCAGCGGTTCTGGCTTCATCATGTCAGAGCGGCGCTGATC 1211
Db      118  AlaAspAspGlyGlyLeuAsnPheGlySerGlyPheIleIleSerLysAsnGlyTyrIle 137
Qy      1212  ATCACCAATGCGCACGTGGTGTCCAGCAACAGTGTGCCCCGGGAGGAGCAGCTCAAG 1271
Db      138  LeuThrAsnThrHisValValAla-----GlyMetGlySerIleLys 151
Qy      1272  GTGCAAGCTTACAGATGAGGAGCTCTCTATGAGGCGCACCATCAAGAAGATGACAGAAGTGG 1331
Db      152  ValLeuLeuAsnAspLysArgGluTyrThrAlaLysLeuIleGlySerAspValGlnSer 171
Qy      1332  GACATTGGCACCATCAAGATCCATCCCAAGAAAAAGTCCCTGTGTTGCTGGGATCAC 1391
Db      172  AspValAlaLeuLeuLysIleAspAlaThrGlnGlnLeuProValValLysIleGlyAsn 191
Qy      1392  TCGGCGGACCTGGCGCTGGGAGATTGTGTGGTGCATCGGACGTCCCTGGCCCTACAG 1451
Db      192  ProLysAsnLeuLysProGlyGluTyrValAlaAlaIleGlyAlaProPheGlyPheAsp 211
Qy      1452  AACACAGTGAACAACGGGATGTCAGACACTGCCACGGGAGGAGGAGGAGTGGGCTTC 1511
Db      212  AsnSerValThrAlaGlyIleValSerAla-----LysGlyArgSerLeuPro--- 227
Qy      1512  CGGAGCTCCGACATGATGATCAAGACGAGATGCCATCAATCACTACGGGAACTCCGGG 1571

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Db 228 AsnGluSerTyrThrProPheIleGlnThrAspValAlaIleAsnProGlyAsnSerGly 247
QY 1572 GGACCACTGGTGAACCTGGATGGAGAGTCAATTGGCTCAACAGCTCAAGGTCACG--- 1628
Db 248 GlyProLeuPheAsnLeuLysGlyGlnValValGlyIleAsnSerGlnIleTyrSerArg 267
QY 1629 -----GCTGGCATCTCCTTGGCATCCCTCCAGACCGCATCACAGGTTCTCTC 1676
Db 268 SerGlyGlyPheMetGlyIleSerPheAlaIleProIleAsp---ValAlaMetAsnVal 286
QY 1677 ACAAGATTCCAGACCAAGACAGATCAAAAGACTGGAAGAGCGCTTCATCGGCATACGAGATG 1736
Db 287 AlaGlu---GlnLeuLysAsnThrGlyValValGlnThrGlyGlnLeuGlyValIleIle 305
QY 1737 CGAAGCATCACACCAACCTGGTGGATGAGCTGAAGGCGACCAACCGGACTTCCAGAG 1796
Db 306 GlnGluValSerTyrGlyLeuAlaGlnSerPheGlyLeu-----Asp 319
QY 1797 GTCAGCAGTGAATTTATGTGACAGAGTGGCGGCAATTCACTTCTCAGAGAGCGCG 1856
Db 320 LysAlaSerGlyAlaLeuIleAlaLysIleLeuProGlySerProAlaGlnThrAlaGly 339
QY 1857 ATCCAGATGCTGATCATCATGTCTCAAGGTCAACGGGCGCTCTTATGATGATCGAGTGA 1916
Db 340 LeuGlnAlaGlyAspIleValIleuSerLeuAspGlyGlyGlnIleArgSerSerGlyAsp 359
QY 1917 CTGACAGAGCCCTG-----CTGACCGAG-----TCTCTCTCTCTCACTGAG 1958
Db 360 LeuProValMetValGlyAlaIleThrProGlyLysGluValSer---LeuGlyValIleTyrPar 379
QY 1959 GTGCGCGGGGGGAACGACGACCTCTCTGACGATCGACGATGAGTGTCAATGAGAG 2018
Db 379 GlyValGlyGlnGluIleThrIleLysAlaLysIleuGlyAsn----- 392
QY 2019 GCGCATCTCTCAAGCGCAAGCTCAGAGCTTGACGACCAACGAGGAGCGCCCGCCCG 2078
Db 393 -----AlaIleGlnIleThrGlyAlaIleSerSerLysThrAspGlnIleProTyrTh 409
QY 2079 AGATCAGAGAGAGGACCAACCGCTCGTGC-----CTGACGAGGCGCGC 2120
Db 409 rGluGlnGlnSerGlyThrPheSerValGluSerAlaGlyIleThrLeuGlnThrIleTh 429
QY 2121 AGCCTCTCTCTG-----CTGTCCGGGCGAGAGCGAGGCTGAG 2159
Db 429 rAspSerSerGlyLysHisLeuValValValArgValSerPheAlaIleGlnThrArgAla 449
QY 2160 CTTGGCCAGGCGC 2172
Db 449 yLeuArgArgGly 453

RESULT 9
US-10-454-437-56
; Sequence 56, Application US/10454437
; Publication No. US2005027115A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Krogger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; FILE REFERENCE: BGI-128CPN
; CURRENT APPLICATION NUMBER: US/10/454,437
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09

; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 56
; LENGTH: 441
; TYPE: PRF
; ORGANISM: Corynebacterium glutamicum
US-10-454-437-56
Alignment Scores:
Pred. No.: 1.67e-16 Length: 441
Score: 387.00 Matches: 127
Percent Similarity: 43.9% Conservative: 66
Best Local Similarity: 28.9% Mismatches: 128
Query Match: 6.9% Indels: 119
Gaps: 17
DB:
US-10-617-443B-1 (1-3006) x US-10-454-437-56 (1-441)
QY 794 AGCCGACGATGGAAGCTTTTAAACATTCGCG-----GATGAG 835
Db 19 ThrProSerGlnThrAsnSerPheGlnHisValArgSerTyrProGlnTrpGlyAsn 38
QY 836 CGAGCCCTTCCCAAAATGCTGTGTCTGACCTGCTGTGTGTGAGGAGGATCCCAACG 895
Db 39 ThrAlaSerAsnGlnAsnPro-----TyrProGly 48
QY 896 GGCTCAGTGTGGGCTGAGGCTGCTCTGAACCTGGACAGAGGCTCTCAGAGAGGCTCTCT 955
Db 49 AlaGlyPheGlySerGlnGlnAsnThrGln-----GlnGlyAsnGlnGlnAlaPro 66
QY 956 CCTCTGCCCCACTGGGATAGGCTCTGAGAGCTGGAGCATCGATCTCACTGATGCA 1015
Db 67 Ala-----TrpThr-----SerTrpAsnGlnProLeuSerThrAsp 79
QY 1016 CCTGCTCTTCCCGCCAGCGCAG----- 1039
Db 80 ValLysProAlaLysGlnLysArgLysValGlyIleGlyThrAlaLeuAlaMetLeu 99
QY 1039 ----- 1039
Db 100 ValGlySerIleAlaThrGlySerValValGlyValAlaAlaThrGlnLeuGlySerAsp 119
QY 1040 ---TCTCCACGACT-----GAGCAGCCCGGCTTACAGTTCAACTTCATTGCTGA 1087
Db 120 SerSerThrProValAsnAlaLeuGlnInProSerValGlnArgThrThrAsn-AlaGly 139
QY 1088 C-----GTGTGAGAGAGTCCACCAAGCGCTGTGTCACATGAGCT 1129
; :
Db 139 uproGlySerAlaGlnGlnValAlaAlaValLeuProSerValIleSerIleGlnAla 159
QY 1130 CTTCGTGAGACACCGGCTGTTGGCGGAGCGCCCTGTCCAGCGGTTGCGCTCAT 1189
Db 159 alleThrArg-----ThSerAlaSerGlnGlySerGlySerI 172
QY 1190 CATGTCAAGAGCGGCTGATCATCAACATGCCAGTGTGTCTCAGCAACAGTGTGC 1249
Db 172 eIleSerSerAspGlyTyrValMetThrAsnHisValAla----- 187
QY 1250 CCGGCGCAGCGCAG-----CTCAAGTGCAGTCAAGATGGGAGCTCTTATGA 1300
Db 188 ----GlyIleGlnGlnSerGlyValLeuGlnValSerPheSerAspGlyThrThrAlaGly 206

[illegible]

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: Sequence 33, Application US/11186284
: Publication No. US20050266493a1
: GENERAL INFORMATION:
: APPLICANT: Millennium Pharmaceuticals, Inc.
: APPLICANT: Berger, Allison
: APPLICANT: Guillemette, Tracy L.
: APPLICANT: Kamatkar, Shubhangi
: APPLICANT: Schlegel, Robert
: APPLICANT: Monahan, John E.
: APPLICANT: Thibodeau, Stephen N.
: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
: TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
: TITLE OF INVENTION: THERAPY OF COLON CANCER
: FILE REFERENCE: MEM01-029P2RNM
: CURRENT APPLICATION NUMBER: US/11/186,284
: CURRENT FILING DATE: 2005-07-21
: PRIOR APPLICATION NUMBER: US/10/301,822
: PRIOR FILING DATE: 2002-11-21
: PRIOR APPLICATION NUMBER: US 60/339,971
: PRIOR FILING DATE: 2001-12-10
: PRIOR APPLICATION NUMBER: US 60/361,978
: PRIOR FILING DATE: 2002-03-05
: PRIOR APPLICATION NUMBER: US 60/381,988
: PRIOR FILING DATE: 2002-05-20
: NUMBER OF SEQ ID NOS: 228
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 33
: LENGTH: 1466
: TYPE: FRT
: ORGANISM: Homo Sapiens
: US-11-186-284-33

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Alignment Scores:	
Pred. No.:	8.77e-12
Score:	309.00
Percent Similarity:	30.2%
Best Local Similarity:	23.6%
Query Match:	5.5%
DB:	7
	Gaps:
	45
	Length:
	1466
	Matches:
	238
	Conservative:
	67
	Mismatches:
	362
	Indels:
	342
	Gaps:
	45

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US-10-617-443B-1 (1-3006) x US-11-186-264-33 (1-1466)
QY 139 CAGCCAGGCCAGCCGAAACCCCTGCTGTGTGTGACAGCCCCAGCCAGTGTCTATTGCGG 198
Dp 208 G1A1aG1yProserG1yPro-----ProG1yProProG1yA1a11eG1y 222
QY 199 GCTCGGGAGCAGAGAGCGCTGACAGACATGTGTTCCAGATGNG1GGGAACTGCGAGAG 258
Dp 223 ProserG1yProA1aG1yLys-----A1aG1yG1uSer 233
QY 259 GCCCGG-----CAGAGCCCGTGCAGAGAAACCCGAGGCGCTGAGCCCC 303
Dp 234 G1yA1rProG1yA1rProG1yG1uA1rG1yL1eA1rProG1yL1eLysG1yPro 253
QY 304 GTGCCACTGCATCCTCAGGCGCTGTGTCTGTGCTGACAGCAGACAGCCCTTACTGTCAGCGCA 363
Dp 254 -----A1aG1yL1eProG1yPhe-----ProG1yMeLysG1yA1s 265
QY 364 GCAGAAATCTGACCCGCGGAGGGGTCCAGG--GAAGTTCGTGAACATCTAGACAGTGC 420
Dp 266 A1rG1yL1PheA1rG1yA1rG1yA1rG1yL1uLysG1yL1uThG1yA1aProG1yL1eLysG1y 285
QY 421 GGCTGGGCTGTGGCCAAAGTTAGACACAGATGTAGGGCCCTGTGACTCAGAAATTGGCAG 480
Dp 286 G1uA1mG1yL1eA1rProG1yG1uA1mG1yA1aProG1yL1ProMeLys----- 300
QY 481 CTCTTTTGGCCAGAGGGGCGACGCTGTGTCTCGGGGCTGGGTAAGTCAAGAAAGGTCACT 540
Dp 301 -----ProA1rG1yA1a-----ProG1yG1uA1rG1yA1rProG1yL1eA1rPro 314
QY 541 GGG-----GGTCTTCCACTACAC 558

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Db 315 GIYAlaLaaglyAlaarglyAaenapglyAlaarglySerapglyInProglyPro 334
 QY 559 CCCCCTGAGACAGCTGCTAGCCCGAGGGCTCGAGGGACCAAGCTGGAGCCCATAGAGA 618
 Db 335 Progly-----ProProglyThraaglyPheProglySerProglyAla 349
 QY 619 GAGGCGACATTCCTCTGTAAGGGATATGCTAGCATGAGGGACACAGAGGCCAG 678
 Db 350 LySgLygluValGlyProAlaagly-----SerProglySerenGlyAlaPro 365
 QY 679 GGGAGCAACCCGAGATCCAGCCCGGCTCACTCCGTTGGCTCAGCGCAATATCTTA 738
 Db 366 GlyInaarglyGluProglyProglyInglyHis----- 376
 QY 739 ACCTCTCTGAGCCCTCTGCCCCAGCTTACAGGCTTCAGTGAAGGGGGTGAAGAGCC 798
 Db 377 -----AlaGlyAlaGlnGlyProProglyProPro-GlyYlaaenGlySerPr 392
 QY 799 AGCAGGTGAGACCTTTTAACCATTCCTGCGGTGAGCGAGCCCTTCCCAATGCTCG 858
 Db 392 oGly-----GlyLySgLygluMetGlyProAlaGlyYleProAl 405
 QY 859 TGTCACTGACTGCTGTGTGTAGGGG-----TCCCAACGGGCTCAGTGTGGCTGA 912
 Db 405 YAlaProglyLeuMetGlyAlaarglyProProglyProAlaGlyAlaenGlyYlaPr 425
 QY 913 G-----GCTGGCTTGAAGCTGGAGCAGGGGCTTCAGAGAAAGCCTCTCTC 957
 Db 425 oGlyLeuAarglyGlyAlaGlyGluProglyLySaenGlyAlaLySgLygluProglyPr 445
 QY 958 TCCCTGCCACTGGGCAATAGGCC----- 979
 Db 445 oArgGlyGluAarglyGlyAlaGlyYleProglyYAlaProglyYAlaLySgLygluAapGly 465
 QY 980 ----TCTGGAGCTGGCAGCATGATCTCATGATGCACTGACCTGGCTTCCCGCAGCG 1035
 Db 465 YLySaapGlySerProglyGlyuProglyYAlaenGlyLeuProglyYAlaLaGlyYleuA 485
 QY 1036 CAGGTCTCCACCAAGCTGAGCAGCCCGCTCAAGTTCAAGTTCAAGTTGCTGACGTGT-- 1093
 Db 485 GgLyAlaProglyPheAarglyProAlaGlyProAlaenGlyYleProglyGlyuLySgLypr 505
 QY 1094 -GAGAGATGCGACAGCCGCTGTCACATAGAGCTTCCGAGAGACCCGCTGTTG 1152
 Db 505 oAlaGlyGluAarglyYAlaProglyPro-----AlaGlyProAarglyYAlaLa----- 521
 QY 1153 GCCGCAACGTGCCCTCTGTCAGCGGTTCTGCTTCATGTCAGAGCGCGGCTGATCA 1212
 Db 522 -----GlyGluProglyA 526
 QY 1213 TCACCAATGCCACGTGTGTCTCAGCAACAGTGTCTCCCGGCGAGGCGAGCTCAAG 1272
 Db 526 gAapGlyValProglyGlyProglyYMetAarglyMetProglySerProgly-----G 544
 QY 1273 TGCAGTACAGATGAGGGAGCTCTTAAGAGCCACCACTCAAGCATCAGCAAGAAAGTCGG 1332
 Db 544 YProglySerAap--GlyLySaPro--GlyProProglySerGlnGlyuSerGlyAarg 562
 QY 1333 ACATTCGCAACATCAAGATTCATCCCAAGAAAAGCTCTGTGTGTGTGCT----- 1384
 Db 563 ProglyProProglyProSerGlyProAarglyGln-ProglyYAlaMetGlyPheProgl 582
 QY 1385 -----GGGTCACTGGCGGACCTGGCGGCTGGGAGTTGTGTGTGCCA 1428
 Db 582 YProLySgLyAaenAapGlyAlaProglyLySaenGlyGluAarglyGlyProglyGlyPr 602
 QY 1429 TCGGAGTGTCTTCCGCTACAGAACACAGTGAACAGGGCATCG-----CA 1476
 Db 602 oGlyProGlnGlyProProglyLySaenGlyuInthrglyProGlnGlyProProglyPr 622
 QY 1477 GCATGTCGACGCGAGGAGGCAAGGA-----GCTGGGCTTCCGGAATTCGACATGAGACTACA 1533
 Db 622 oThrglyProGlyGlyAapLySgLyAapThrglyProProgly----- 636

QY 1534 TCCAGACGAGTGCATCATCACTACGGAACCTCCGGGGGACCACTGTGAACCTTGANG 1593
 Db 637 -ProGlnGly-----LeuGlnGlyLeuProglyYInthrglyYleProProglyYgl 652
 QY 1594 GCGAGGTCAATTGGCATCAACAGCTCAAGGTCAAGCTGGCATCTCTTGGCATCCCT 1653
 Db 652 uAenGly----- 654
 QY 1654 CAGACCGCATCAACAGGTTCTTCAAGAGTTCCAAAGACAGCATCAAGACTGGAA 1713
 Db 654 ----- 654
 QY 1714 AGCGTTCAATGGGCAATGGAGATGGAGATCAACAGCCCTGTGATGAGCTGAAG 1773
 Db 655 -----LySProgly----- 657
 QY 1774 CCAGCAACCCGAGCTTCCAGAGTCAAGCATGGAATTTATGTGCAAGAGTTGCGCGA 1833
 Db 658 ----GluProgly-----ProLySgLy----- 663
 QY 1834 ATTCACCTTCTCAGAGAGCGGCAATCAAGATGTGATCATCTGTCAAGGTCAACGGC 1893
 Db 663 ----- 663
 QY 1894 GTCTCTAGTGAAGTGAAGTGAAGTGAAGAGCGGCTGACCGAGTCTCTCTCTAC 1953
 Db 664 ----AapAlaGlyAlaProglyYAlaProglyYLySgLyAap----- 676
 QY 1954 TGGAGGTGCGCGGGGGAACGACGACTCTCTTACGATCGACCTGAGTGTGATGT 2013
 Db 677 -AlaGlyAlaProglyGlyuAarglyProPro----- 686
 QY 2014 GAGGGGCGCATTCCTCAGCGGCAAGCTCAAGCTGCAACCAAGAGGCGAGCGCC 2073
 Db 687 -----GlyLeuAlaGlyAlaProglyYleuAarglyYAlaGlyPr 700
 QY 2074 CCCCAGATCAAGAGAGACCACTCGGTCTCAGAGGGGCGGACCTCTCTCTG 2133
 Db 700 oPro-----GlyProGlnGlyYlySgLyAlaLaGlyProProglyProProgl 717
 QY 2134 CTGTCCGGGCGAGAGCGAGCTGGCTTGGCCAGAGGCGCGAATTTCCGCTGGGAGT 2193
 Db 717 YAlaLaGlyYInthrglyProglyYleuGlnGlyMetProglyYleuAarg-----GlyGlyLe 734
 QY 2194 GTTGATTCACATCCCGGTGCGGGAGGGAAGCCCAACATCCCTTGTACAGATATCC 2253
 Db 734 uGlySerProglyProLySgLyAapLySgLygluProglyGlyProglyYAlaAapGly-- 753
 QY 2254 TGAAGTCACTTCCAAATTCCTCCGATATTCACAAAACCTCTTCATGAGAGTCCCC 2313
 Db 754 -----ValProglyYLySaapGlyProA 761
 QY 2314 CTCTCTAGC-----TTCGCGCTTGGCCCTGTGAACACCATCTGACATGATCC 2364
 Db 761 GgLyProthrglyProGlnGlyProPro-GlyProAlaGlyInProglyYLySgLy 781
 QY 2365 CTGTCTTGGCTCTCTACTGAGATCTGGGCTGGCCAAAGCTTCTTCCCTGACAAAG 2424
 Db 781 LuGlyYAlaProglyLeuProglyYleAlaGlyProAarglySerProglyYluAarg 801
 QY 2425 CCCACTGACCTGAAGGCGGCGAGCTTCCCTGAGCTTCAAGACTTAAGGCGC- 2483
 Db 801 YgluThr-----GlyPro-----ProglyProAlaGlyPheProglyYAlaProglyG 817
 QY 2484 -----AGGCTGTGCTCT 2496
 Db 817 LlaenGlyluProglyGlyLySgLyAarglyYAlaProglyYgluLySgLygluGly 837
 QY 2497 GCGACCTGGGGCTC-----CTTGAGAGCAGGTCACTGATCTCTTGGGGCTC 2547
 Db 837 LyProProglyYAlaLaGlyProProglyGlySerGlyProAlaGlyProProglyProgl 857

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QY      2548 GGGCG-----TGGGCTTCAGCCCAAGCAGGCACGTGATGA 2583
           ::|||
Db       857 InglyValIysGIyLurGIySerProGIyGIyProGIy-ALAAlagIyPheProGIy 876
QY      2584 ATG-----CCCCCTGACTTGCGAGCTGAGGCCCGCCCTGACCATGAGTTT 2628
Db       877 ALAatrgGIyLeuProGIyProProGIySeranGIyAnProGIyProProGIyProser 896
QY      2629 TCCTTCCTCCAGCAGCAGAGAGCGCCGCGGGAGACAGTGGAAATTGCTGCTCTGGGG 2688
Db       897 GlySerProGIyLyIyaAsp-GlyProProGIyProAlagIyanthrGIyAla-ProGlys 916
QY      2689 AA-----GCTTCTCTCTCCCAAGCGCGCAATGGGGCAGCTCGCAGAGAGACAGTGAAGT 2742
Db       916 erProGIyValSerGIyProIyPheGIyAsp-ALagIyGlnProGIyGln-----Iys 932
QY      2743 GGAGCTGCGGGGTGTGAGACATGAGCCGAGCTTCCCCTTCACAGACGCTGTGAGATGACG 2802
Db       923 GlySerProGIyAlaGlnGly-ProProGIyAlaProGIyProleuGIyIleAlagIyII 952
QY      2803 CAGCGCGCTGCGATGGAGATGGCCGCCACAGAGCATGACAGGCTGCTGGCACCACTCCCTCA 2862
Db       952 eThrGIyAlaArgGIyLeuAla-----GlyProProGIyIyme 964
QY      2863 TCCAGAG 2869
Db       964 cProGIy 966

RESULT 14
US-10-821-234-964
; Sequence 964, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;   APPLICANT: Labat, Ivan
;   APPLICANT: Stache-Crain, Birgit
;   APPLICANT: Andarmani, Susan
;   APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIORITY FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 964
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-964

Alignment Scores:
Pred. No.:          7,38e-11              Length:         1166
Score:             293.50                 Matches:          224
Percent Similarity: 30.4%                  Conservative:     60
Best Local Similarity: 24.0%                Mismatches:       340
Query Match:        5.3%                   Indels:           311
DB:                  6                     Gaps:            43

US-10-617-443B-1 (1-3006) x US-10-821-234-964 (1-1166)
QY      139 CAGCCAGGCCAGCCGAAACCCTGGTGTGTGCAGACCCCAAGCCCAAGTTGCTCATTTGGCGG 198
           |||||||:::|||
Db       211 GlnlagIyProserGIyPro-----ProGIyProProGIyAlaIIegIy 225
QY      199 GCTCGGAGCCACAGCAGAGCGGTGACGACATGTGTTCCAATAGTGGAACTGAGAGA 258
           |||:::
Db       226 ProserGIyProAlaGIyIyb-----AspGIyGIusSer 236
QY      259 GCCCGG-----CACAGCCCGTGCAGAGGAACCCGAGAGGCTGTAGGCCCC 303
           |||:::|||
Db       237 GIyAtrgProGIyArgrProGIyGIyLurGIyLeuProGIyProProGIyIIleIyegIyPro 256

```

QY	304	GTGCCACTGCATGCTCAGAGCGCTGTGTCTGTGACGCCACAGCGCCCTTACTGTACGGCA	363
Db	257	-----AlaGlyLeuProGlyPhe-----ProGlyMetGlyHis	268
QY	364	GCAAGAAATCTGAGCCCGGGAAGAGTCCAGG---GAAATTCTGAAACATCTGACAGTGG	420
Db	269	ATgTgLYPheAPGlyYARgAnGlytGlyuYbGlytGlytHrGlyYAlaProGlyLeuYbGly	288
QY	421	GCGTGGGTGTGGCCCAAGTTTGAACAAGATGTAAAGGCGCTGTGTGACTCAGAAATTGGCAG	480
Db	289	GIuAnGlyLeuPProGlyGIuAnGlyAlaPProGlyPProMetGly-----	303
QY	481	CTCTTTTGGCCCAAGAGGGCCACGCTGTGTCCGGCGCTGGGTAGCTCAGAGGGTCACT	540
Db	304	-----ProArgGlyYala-----ProGlyGIuArgGlyYARProGlyLeuPro	317
QY	541	GGG-----GCTTTCACCTACAC	558
Db	318	GIYAlaAlaGlyYAlaArgGlyYAnAPGlyYAlaArgGlySerAPGlyYAlnProGlyPro	337
QY	559	CCCCCGCTGACACATGCTGTAGCCCCCAGGGGCTCGAGAGGACACAGCTGAGCCATAGAGA	618
Db	338	ProGly-----ProProGlytHrAlaGlyPheProGlySerProGlyYala	352
QY	619	GAGGGCCAGTTCTCTCTGTAAAGGTATTGTCTGATGACATGAGGAAACAGACAAAGCCGAC	678
Db	353	LybGlytGlyuAlGlyProAlaGly-----SerProGlySerAnGlyYAlaPro	368
QY	679	GGGAGCTAACCCGAAATCCAGCGCCCGGCTCACTCCCGTGTGGCTCACGGCAATATCTTA	738
Db	369	GIYGIuARgLyGlynPProGlyProGlnGlyYAs-----	379
QY	739	ACCTCTCTGTAGCTCTCGCCACGCTACAGAGGCTCAGTGAAGGGGTGAGAAAGCC	798
Db	380	-----AlaGlyYAlaGlnGlyProProGlyProPro-GlyYIleAnGlySerPr	395
QY	799	AGCAGGTGAAGCCCTTTTAAACATCTTCGGGGTGAAGCGAGCCCTTCCCAATAGCTGG	858
Db	395	CGly-----GlyYbGlytGlyMetGlyProAlaGlyYIleProGly	408
QY	859	TGTCACTGCATCTGCTGTGTGTGATGGGG-----TCCCAACGGGCTCAGTGTGGGCTCA	912
Db	408	YAlaPProGlyLeuMetGlyYAlaArgGlyProProGlyProAlaGlyYAlaAnGlyYAlaPr	428
QY	913	G-----GCGGCTCTGAACTGGGACAGAGGGGTCTCAGAAAGAGCTCTCTCC	957
Db	428	CGLYLeuARgLyGlyYAlaGlyGlynPProGlyYLYbAnGlyYAlaYbGlyGlynPProGlyPr	448
QY	958	TCTCTGCCCATGGGCGATAGGCC-----	979
Db	448	CArGlyGlyGIuARgLyGlytGlyuYAlaGlyYIleProGlyYAlaProGlyYAlaYbGlyGIuAnPGL	468
QY	980	----TCTGGAGCTGGGACAGCATCGTGAATCTCACTGATGCACCTGGCCCTTCCCGCCAGCG	1033
Db	468	YLYbAnPGLySerProGlyGIuPProGlyYAlaAnGlyLeuPProGlyYAlaAlaGlyGIuAR	488
QY	1036	CAGGCTCTCCACACGCTGAGCAGCGCCGCGCTACAAATTCAACTTCACTTGTGACGTGGT--	1099
Db	488	gGlyYAlaPProGlyPheARgLyProAlaGlyYProAnGlyYIlePProGlyGlyuLYbPPr	508
QY	1094	-GGAAGAAATGCAACAGCCCGTGTGTCCACATAGAGCTCTTCTCTGAGACACCGCTGTGGT	1155
Db	508	CAAGlyGIuARgLyGlyYAlaPProGlyPro-----AlaGlyYProARgLyYAlaAla-----	524
QY	1153	GCCGCAACGTGCCCTGTTCAGCGGTTCTGCGTTCAATGTCAGAGCGCGGCTGTATCA	1211
Db	525	-----GlyGIuPProGlyYAR	529
QY	1213	TCACCAATGCCACAGTGTGTTCAGCAACAAGTCTGCCCGGGGACGACAGCTCAAGG	1277
Db	529	gAPGlyYAlaPProGlyGlyYProGlyMetARgLyYMePProGlySerProGlyY-----GI	547
QY	1273	TGCAGCTCACAATGGGGACTCTTATGAGGGCCACCATCAAGAGCACTCACAAGAGTGGG	1333

[illegible]

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Db      764  gdlpProthrntelgProIleelgIyProPro-gIyProIalagIyblnProglYasbIyglYg 784
QY      2365  CTGCTCTGCTCCCTCTCTACTGCAAGCTCTGGGGCTGCCAAGCTTCTTCCCTCGACAAG 242
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Db      784  lUGlYglYAlAProglYleuProglYleIleaglYProArgIySerProglYgluArg 804
QY      2425  CCCACCTGAACCTGAAGGCCCAAGCTTCCCTCTGCCCTAGAGACTTACCAAGCTGAAGGCCA 248
           |||||
Db      804  lYgluThr-----glYPro-----ProglYProIalaglYpHePro----- 815
QY      2485  GAGCTCTGCTGCTCCGACCTGGGGCTGGGGCTCTGGAGAGACATCATCTGATTCCTTTGGGG 254
           |||||
Db      816  --glYAlAProglYglInamntelYgluProglYglYlYglYgluArgIyAlAProglYg 835
QY      2545  TGGCGGGGTGGGGT-----CGAGCCAGACAGGCACTAGTGAATGCTCCCT----- 259
           |||||
Db      835  lulYsGlYglUGlYglYProProglYVal-AlagIY-----ProProglYlYs 850
QY      2553  ---GGCTGGAGAGCTGAAGCCCGCCCTGCAATGAGTTTCTCCCTCCAGGACGAGAG 264
           |||||
Db      851  AsbglYThrSerIglYAlAProglYProIleglYProProglY-ProIArgIYAsbArgI 870
QY      2650  GCCCGGGGAGAGACAGCTGGAAAGTTGGCTGCTGCTCGGGGACCACTTCTCTCT----- 270
           |||||
Db      870  YgluArgIySerIglYglYSerProglYhIb-ProglYglInProglYProProglYPro 890
QY      2704  AAGCGGCAATGGGGGCAAGCTGCAAGAGA 2732
           |||||
Db      890  rogIYAlAProglYProCybGslYglY 899

RESULT 15
US-11-182-016-23
; Sequence 23, Application US/11182016
; Publication No. US20060019294A1
; GENERAL INFORMATION:
; APPLICANT: SUGEN, INC.
; TITLE OF INVENTION: TYROSINE KINASE SUBSTRATE (TKS) PROTEINS
; FILE REFERENCE: 038602/0102
; CURRENT APPLICATION NUMBER: US/11/182,016
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US/09/958,359
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 1742
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Grub
US-11-182-016-23

Alignment Scores:
Pred. No.: 6,93e-10 Length: 1742
Score: 277.50 Matches: 273
Percent Similarity: 33.3% Conservative: 113
Best Local Similarity: 23.5% Mismatches: 426
Query Match: 5.0% Indels: 349
DB: 7 Gaps: 62

US-10-617-443B-1 (1-3006) x US-11-182-016-23 (1-1742)
QY      24  TCCACACTCAGTTCCTCCACAGATGTGGT---AGGAGGCAATATTCAGTCCATTTTTCAGA 80
           |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      396  SerleuSuAenAArgArgArgCySerIyArgIySerThrTPArgArgHIshePheArg 415
QY      81  -----TGAGAGTGGAGGCCCAAGAACTGAATGATCTGTCTGAG---CCACACAGC 131
           |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      416  ProglInMetThrValIyglYSerArg-----CyIySerCyabProCySer 431
           |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      132  TAGAAAGACAGCAGGCCCAAGCCGAACCCCTGTGTGTGTCAG-----CCCAAGCC 182
           |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      432  PheArgSerIleSerGlInProArgThrAlaSerThrAlaSerArgSerleuProArgAla 451
           |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

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QY	183	AGTTGCTATTCCGGGAGCTCGGAGACCAAGCAGAGGCTGACAGACATGTTTCCAGATG	242
Db	452	SerCySer-----ArgSerSerCyThralaalaProArglaaRHis-----Serlu	468
QY	243	GGGGAACCTGAGAGAGCCGGGACACAGCCCGCTGCAGGAGAC-----	284
Db	469	LeuSerSerGly-----ProIaSerLeuArgSerSerSerSerArgProIyArg	486
QY	285	-----CCCGAGGGCTGT-----AGGCCCGTGCACTGCATGCTCCAGGCT	326
Db	487	ValSerCySerSerArgGlyCySerArglaaArgGlyArgGlyProIaSerMetGluPro	506
QY	327	GNGGTC-----CTGGCAGCCACAGAGCCCTACTGCTGACGGAGAGAG-----	368
Db	507	LeuLeuLysGlyLeuSerSerIaIaIaArgProPheSerSerLeuCyArgGlyCysPheThrTy	526
QY	369	-----AATCTGAGCCCGGGAGAGGTCACAGGAGAGTTCGTGAACCATCTTAGCA	416
Db	527	CysIaIaArgLeuAsnThrSerProItrPArgArgLys-----Gln	539
QY	417	GTCGGGCTGGGGTGTGGCCAAGTT-----AGCACACATGCT-----	452
Db	540	AlaProMetArgArgGlyTyrPValIaGlnProSerSerArgLysPheCysValArgTyr	559
QY	453	-----AGGGCCCTGTGTGACTGCAAAATTGGAGCTTTTGGCCAG	494
Db	560	LysLeuArgSerLeuSerArgIaIaLeu-----ArgAlaIaIaGlnValProArg	576
QY	495	AGGGGCCACGCTGTGTCGGGGCTTGGAAGCTCAGAAAGGTCACCTGGGGGCTTTCAC	554
Db	577	SerSerGlyValSerSerGlyProGly-----GlyGlyThyGly	589
QY	555	ACACCCCGGCTGGAACACTGCTGTAGCCCCAGGGCTCGAGGGAC-----	599
Db	590	SerLeuLysValAlaThrSerCySerGlnAlaIaSerSerAspThrSerArgCysTrp	609
QY	600	-----CAGCTGAGCCCATGAGAGAGGGCCAGTTCTCTCTGTAAAGGTATT	647
Db	610	AlaLeuMetLeuArgLeuArgSerIleArgGlyIaPro-----	622
QY	648	GCTGTAGCATGAGGGAACAACAAGAGCCCAAGGGGAGCTAACCCGAGATCCAGCCCCGCC	707
Db	623	-----ThrProGlnIlyProSerGlyProLeuAlaArgPro-----	634
QY	708	TCACCTCCGCTGGGCTCACGGCAGATAT-----	734
Db	635	SerSerThrCysSerArgGlyIuIuIuIuValLeuSerThrThrSerValLeuValThrSer	654
QY	735	---CCTAACTCTCTCTGAGCCTC-----CTGCCAGCTAGCAGAGGCTCAGTGAGGGG	785
Db	655	ArgProArgIleSerThrAlaLeuGlyLeuProSerAlaSerGlyAlaSerSerGly	674
QY	786	GGTAGGAAGCCACAGCAGTGSAAACCTTTTAACATTTCTGGGGTAGAGAGCCCTT	845
Db	674	-----	674
QY	846	CCCAATGCTGGTGTCTACTGCACTGCTGTGTAGGGGGTCCCAACAGGCTCAGTGT	905
Db	675	ProSerSerSerSerSerProHis-----	682
QY	906	GGGCTGAGAGGCTGGCTCTGTAACCTGGGACAGGGGTCTCAGAGAGGCTCTCTCTGCCC	965
Db	683	GlyAlaArg-----GluGlnTyrAspGlyAlaGlyArgGlyProGlyLeuLeuLysSer	700
QY	966	ACTGGGCAATGAGCCTCTGGAGAGCTGAGAGCATGATCTCACTAGTCACTGGCCCTT	1025
Db	701	SerLysGluLeuArgLeuGlyIuIuIu-----LeuArgGlyProHis--TyrAla--	716
QY	1026	CCCGCCAGCGCAGGTTCTCCACAGCTGAGACGCCCGCGCTACAGTTCAAGTTCAATTGCT	1085
Db	717	ProPro-----LeuLeu	720

QY	1086	GACGTGGTGGAGAAAGATGCACCAAGCCGTGTGTCCACTAAGACTCTTCTCTGAAGACACCG	1145
Db	720	uAlaProSerAlaArgArgArgArgProArgGlyLeuAlaSerSer	ProAr 737
QY	1146	CTGTATGGCCGCAACGTGCCCCCTTCACGCGGTTCTGGCTTCATCATGTACAGAGCCGCG	1205
Db	737	gCyS-----CyStrpIleLeuLeuSerSerStrpIlnArg	749
QY	1206	CTGATCATCACAATGCCACAGTGTGTCCAGCAAGTGTCTGCCCGGCGAGCAGAC	1265
Db	750	----AlaTrpIlnArgProIlnSerAlaArgAlaAlaGlyLeuProArgSerArgAlaAr	768
QY	1266	CTCAAGGCGCATACAGA-----ATGGGGACCTCATAGAG-----CCACC	1307
Db	768	gAlaArgIleSerTrpIlySerValProAlaLeuGlySerGlyValAlaArgArgAlaSerAl	788
QY	1308	ATCAAGAATCATGACAAGAAGTCCGACATTCGCCACATCAAGATTCATCCCAAGAAAAG	1367
Db	788	aAlaSerThrAlaSerThrProGlyProAlaProAlaSerArgAlaIlyProSerSerThr	808
QY	1368	CTCCCTGT	1427
Db	808	rHisSerCyAlaCySerTrpIlyIlySerG-----CySerArgArgAlaArgTrpArgPr	826
QY	1428	ATCGGACATGCTCTTCTCGGCTTCACAGAACAGATGCAACAGGAGCATCTGCA-----	1476
Db	826	oleuSerThrCySerSer-----SerArgCySerIlyIleSerSerThrProIlnArg	843
QY	1477	----GCATCGCCCAAGCGGAGGCGAGGAGCTGGGGCTCCGGGACATCCGACATGACATAC	1532
Db	843	uValAlaIlePheSerSerArgAlaArgAlaSerArgAlaTrpAlaArgArgSerTrpThrSe	863
QY	1533	ATCC-----ATCC-----ATCC-----ATCC-----ATCC-----	1536
Db	863	rAlaLeuIlyAlaIArgAlaArgAlaArgSerValSerCyArgAlaAlaArgIlyValSerProG	883
QY	1537	----AGACGATGCCATCATCATCACTACAGGAAATCCGGGGAGACCATGTGTGAAC--TG	1589
Db	883	yIleAlaIlyLeuAlaSerCySerSerProGlyProGlnSerHicCyAlaAnthrCyStr	903
QY	1590	GATGGCGACAGTCA-----GATGGCGACAGTCA-----GATGGCGACAGTCA-----	1602
Db	903	pSerArgArgArgHicIcyValArgCySerCyValSerThrCyValArgLeuIlyArgArgTh	923
QY	1603	-----TTGGCATCAACACGCTTCAGAGTCAAGGCTGGCATCTCTTGTGCATCC-----	1650
Db	923	rSerTrpMetAlaSerSerThrSerTrpSer-----ValAlaGlyProThrProSerSerIle	942
QY	1651	-----CTTCAGACCGCATATCACAGG	1670
Db	942	uLeuLeuGlyValGlnArgSerLeuIleArgMetAlaProProSerSerLeuCySerAlaIyA	962
QY	1671	TTTCTTCACAGAGTTTCCAAAGACACAGACATCAAAAGACTGTGAAGAAAGGCTTCAGGACA	1730
Db	962	IleArgIlySerAlaSerThrIleCySerGlyLeuGlyIleProThrAlaSerSerSe	982
QY	1731	CGATGCGGACGATCACACCAAGCGCTGTGTGATGACTGATGAAGCCAGCAACCCGGAATTC	1790
Db	982	rSerGlySerAlaIleProSerSerSerSerMetAlaCyArg-ThrGlnProSerThrP	1002
QY	1791	CCAAAGGTCAAGATGGAATTATATGTCCAAAGAGTTGGCGGCAATTCACCTTCCAGAGA	1850
Db	1002	roTrpHicAlaArgArgHicSerLeuThrTrpSerTrpCyAlleSerThrGlnLeuGlyGlnG	1022
QY	1851	GCGCGCATCCCAAGATGTGACATCATCATGTCAAGGTCAACGGGCGTCTCTATGTGACTCG	1910
Db	1022	IySerLeuPro-----ProAlaSerHicIcySerSerSerGlyLeuA	1036
QY	1911	AGTAACTGCACAGAGCGCGTGCAGCAAGTCTCTCTCTACT--GGAAGTGCAGCGG	1967
Db	1036	IaThrIleuPheArgSerPheSerAlaPheThrThrSerAlaProAlaProGlnIlnSerSerValG	1056
QY	1968	GGGAACAGACGCTCTCTTCAGAGTGCACCTGAAGGTGTCAATGTGAAGGGGCGCATTC	2027

Db 1382 ArgGlyProArgProPheTrpCysAlaHisAlaArgCysLeuArgTrpArgPro 1339

[illegible]

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2006, 21:02:06 ; Search time 47 Seconds
(without alignments)
587.525 Million cell updates/sec

Title: US-10-617-443b-2

Perfect score: 1679

Sequence: 1 MHMLPASAGLHQLSSPRK.....LEVRGNDLLFSIAPEVVM 334

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:.*
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:.*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:.*
4: /cgn2_6/ptodata/1/1aa/ECTUS_COMB.pep:.*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:.*
6: /cgn2_6/ptodata/1/1aa/Backfilltest.pep:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1034.5	61.6	323	US-09-949-016-10514	Sequence 10514, A
2	1034.5	61.6	447	US-10-104-047-2765	Sequence 2765, Ap
3	1034.5	61.6	480	US-09-949-016-6270	Sequence 6270, Ap
4	1027.5	61.2	480	US-08-923-454A-18	Sequence 18, Appl
5	882	52.5	458	US-08-923-454A-8	Sequence 8, Appl
6	882	52.5	458	US-08-923-454A-25	Sequence 25, Appl
7	882	52.5	458	US-09-008-271A-11	Sequence 11, Appl
8	882	52.5	458	US-09-968-415-11	Sequence 11, Appl
9	882	52.5	529	US-09-075-460-5	Sequence 5, Appl
10	878	52.3	458	US-08-923-454A-31	Sequence 31, Appl
11	862.5	51.4	400	US-09-724-864-55	Sequence 55, Appl
12	779	46.4	436	US-08-923-454A-6	Sequence 6, Appl
13	779	46.4	436	US-08-923-454A-29	Sequence 29, Appl
14	564	33.6	323	US-08-923-454A-27	Sequence 27, Appl
15	564	33.6	323	US-08-923-454A-27	Sequence 27, Appl
16	454	27.0	491	US-09-438-185A-980	Sequence 980, App
17	450.5	26.8	491	US-09-489-039A-13694	Sequence 13694, A
18	441.5	26.3	455	US-09-711-164-416	Sequence 416, App
19	431	25.7	355	US-09-711-164-417	Sequence 417, App
20	428	25.5	460	US-09-199-637A-132	Sequence 132, App
21	425	25.3	475	US-09-252-991A-29494	Sequence 29494, A
22	424	25.3	173	US-08-923-454A-2	Sequence 2, Appl
23	422	25.1	475	US-08-350-741-2	Sequence 2, Appl
24	422	25.1	475	US-08-463-875A-2	Sequence 2, Appl
25	418	24.9	475	US-08-278-091-6	Sequence 6, Appl
26	418	24.9	475	US-08-483-859-6	Sequence 6, Appl
27	418	24.9	475	US-08-472-173-6	Sequence 6, Appl

28	418	24.9	475	1	US-08-487-167-6	Sequence 6, Appl
29	418	24.9	475	1	US-08-482-816-6	Sequence 6, Appl
30	418	24.9	475	1	US-08-296-149-6	Sequence 6, Appl
31	418	24.9	475	1	US-08-801-459-6	Sequence 6, Appl
32	418	24.9	475	1	US-08-615-271-6	Sequence 6, Appl
33	418	24.9	475	2	US-09-074-660-6	Sequence 6, Appl
34	418	24.9	475	2	US-09-074-659-6	Sequence 6, Appl
35	418	24.9	475	2	US-09-106-468-6	Sequence 6, Appl
36	418	24.9	475	2	US-09-106-468A-6	Sequence 6, Appl
37	418	24.9	475	2	US-09-106-467-6	Sequence 6, Appl
38	418	24.9	499	2	US-09-673-898-6	Sequence 6, Appl
39	417	24.8	360	2	US-09-489-039A-13634	Sequence 13634, A
40	415.5	24.7	409	2	US-09-902-540-11885	Sequence 11885, A
41	415	24.7	370	2	US-09-673-898-8	Sequence 8, Appl
42	414	24.7	414	2	US-09-388-090-6	Sequence 8, Appl
43	414	24.7	463	1	US-08-485-569-2	Sequence 2, Appl
44	414	24.7	463	1	US-08-480-993-2	Sequence 2, Appl
45	414	24.7	463	1	US-07-903-079B-2	Sequence 2, Appl

ALIGNMENTS

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RESULT 1
US-09-949-016-10514
; Sequence 10514, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 10514
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10514

Query Match
Best Local Similarity 61.6%; Score 1034.5; DB 2; Length 323;
Matches 203; Conservative 60; Mismatches 55; Indels 9; Gaps 2;

10 GHHQLSSPRYKFNFIADYVEKIPAVVHIEFLRHPPLGRNVPLSSGSGFIWSEAGLIIT 69
1 GQEDNSLRHKNFPIADYVEKIPAVVHIEFLRKLPSKREVPVSSGSGFIWSEGLIYT 60
61 NAAVVTN-----KRAVVEELKNGATYEAKIKDVEKDIALLIKIDHOGKLPVLLIGSS 114
70 NAAVTSNSAAPRQQLVQVONQDSYRATIKDIDKSDIATIKKHPKKLPVLLIGSHA 129
61 NAAVVTN-----KRAVVEELKNGATYEAKIKDVEKDIALLIKIDHOGKLPVLLIGSS 114
130 DLRPGEFVAAGSPALONTYTTGIVSTAOREGRELGLRDSMDYIOTDAIINYNSGCP 189
115 EIRPEFVAAGSPSLONTYTTGIVSTOEGKELGLRNSDMYIOTDAIINYNSGCP 174
190 LVNLDEVIAGINTLKVTAAGISPAISDRITPFLTEFODKQIKD---WKRFIGIMRTIT 246
175 LVNLDEVIAGINTLKVTAAGISPAISDKIKFLTESHRQAKGKAITKKKYGIRMSLT 234
247 PSVLDELKASNDPPEVSSGIYQEVAVANSQKRGIDGDIIVYVNRPLVDSSELDGA 306
235 SSKAKELDRDRDPDVISGAYIIEVPTPAEAGLKENYVITISNGSVSANDVSDV 294
307 VLTSEPLLLEVRGNDLLFSIAPEV 334
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Db 295 IKRSTLNMVVRGNEIMITVPEI 321

RESULT 2

US-10-104-047-2765

Sequence 2765, Application US/10104047

Patent No. 6943241

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION: No. 6943241el full length cDNA

FILE REFERENCE: HI-A0105

CURRENT APPLICATION NUMBER: US/10/104,047

PRIOR FILING DATE: 2002-03-25

PRIOR APPLICATION NUMBER:

NUMBER OF SEQ ID NOS: 4096

SOFTWARE: Patent Ver. 2.1

SEQ ID NO 2765

LENGTH: 447

TYPE: PRT

ORGANISM: Homo sapiens

US-10-104-047-2765

Query Match 61.6%; Score 1034.5; DB 2; Length 447;

Best Local Similarity 62.1%; Pred. No. 1e-102;

Matches 203; Conservative 60; Mismatches 55; Indels 9; Gaps 2;

QY 10 GHHQSSPRKPFADYVEKIAPAVNHIELFLRHPFGKRVPLSSGSGFTMSAGLIIT 69

Db 125 GQEDPNSLRHKYFIADYVEKIAPAVNHIELFRKLPPSKREVPAVSSGSGFTVSEDLIYT 184

QY 70 NAHVSSNSAAPGRQOLKVQLONGDSYEATIKDIDKSDIATIKIPKKKLPVLLGHSA 129

Db 185 NAHVNTN-----KRVKVELKNGATYEAKIKVDKADILIKIHOGKLPVLLGRSS 238

QY 130 DLPRGEFVVAIGSPFALONTVTGIVSTAGREGRELGRSDMDYIQTDAIINYNSGSGP 189

Db 239 ELRPGEFVVAIGSPFSLQNTVTGIVSTAGREGRELGRSDMDYIQTDAIINYNSGSGP 298

QY 190 LVNLDEYIGINTLKTATAGISPAISDRITRFLTEPDQKID--WKRFIGIRMTIT 246

Db 299 LVNLDEYIGINTLKTATAGISPAISDRITRFLTEPDQKID--WKRFIGIRMTIT 358

QY 247 PSVLDELKASNDPPEVSSGIYQEVAPNSPSQSGIODGDIIVKNGRPLVDSSELOEA 306

Db 359 SSKAKELDKRRDPFDVYISGAYIIEVLPDTPAENGKLENDVITISNGSVSANDVSDV 418

QY 307 VLTPSPLLEVRGNDLLFSIAPEV 333

Db 419 IKRSTLNMVVRGNEIMITVPEI 445

RESULT 3

US-09-949-016-6270

Sequence 6270, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6270

LENGTH: 480

TYPE: PRT

ORGANISM: Human

US-09-949-016-6270

Query Match 61.6%; Score 1034.5; DB 2; Length 480;

Best Local Similarity 62.1%; Pred. No. 1.1e-102;

Matches 203; Conservative 60; Mismatches 55; Indels 9; Gaps 2;

QY 10 GHHQSSPRKPFADYVEKIAPAVNHIELFLRHPFGKRVPLSSGSGFTMSAGLIIT 69

Db 158 GQEDPNSLRHKYFIADYVEKIAPAVNHIELFRKLPPSKREVPAVSSGSGFTVSEDLIYT 217

QY 70 NAHVSSNSAAPGRQOLKVQLONGDSYEATIKDIDKSDIATIKIPKKKLPVLLGHSA 129

Db 218 NAHVNTN-----KRVKVELKNGATYEAKIKVDKADILIKIHOGKLPVLLGRSS 271

QY 130 DLPRGEFVVAIGSPFALONTVTGIVSTAGREGRELGRSDMDYIQTDAIINYNSGSGP 189

Db 272 ELRPGEFVVAIGSPFSLQNTVTGIVSTAGREGRELGRSDMDYIQTDAIINYNSGSGP 331

QY 190 LVNLDEYIGINTLKTATAGISPAISDRITRFLTEPDQKID--WKRFIGIRMTIT 246

Db 332 LVNLDEYIGINTLKTATAGISPAISDRITRFLTEPDQKID--WKRFIGIRMTIT 391

QY 247 PSVLDELKASNDPPEVSSGIYQEVAPNSPSQSGIODGDIIVKNGRPLVDSSELOEA 306

Db 392 SSKAKELDKRRDPFDVYISGAYIIEVLPDTPAENGKLENDVITISNGSVSANDVSDV 451

QY 307 VLTPSPLLEVRGNDLLFSIAPEV 333

Db 452 IKRSTLNMVVRGNEIMITVPEI 478

RESULT 4

US-08-923-454A-18

Sequence 18, Application US/08923454A

Patent No. 6004794

GENERAL INFORMATION:

APPLICANT: Creasy, Caretha

APPLICANT: Livi, George

APPLICANT: Kairan, Eric

APPLICANT: Clinkenbeard, Helen

APPLICANT: Browne, Michael

APPLICANT: Southan, Christopher

TITLE OF INVENTION: HUMAN SERINE PROTEASE

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/923,454A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/025436

FILING DATE: 06-SEPT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Baumeister, Kirk

REGISTRATION NUMBER: 33,833

REFERENCE/DOCKET NUMBER: P50547

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-5096

TELEFAX: 610-270-5090

TELEX:
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-923-454A-18

Query Match 61.2%; Score 1027.5; DB 2; Length 480;
Best Local Similarity 61.8%; Pred. No. 6.5e-102;
Matches 202; Conservative 60; Mismatches 56; Indels 9; Gaps 2;

QY 10 GLHQLSPRYKFNFIADVVEKIAPAVNHLEFLRHPLEFGNVPPLSSGSGFIMSEAGLIIT 69
DB 158 GQEDNSLRHKNTFIADVVEKIAPAVNHLEFLRKLPSGRKREVPVSSGSGFVSEDXLIVT 217
QY 70 NAAVVSNSAPARQOLKVQLONGDSYEATIKDIDKSDIATIKIHPKKLPVLLGHS 129
DB 218 NAAVVTN-----KRRVVELKNGATYEAKIKDVEKADIALIKIDHCKLPVLLGHS 271
QY 130 DIRPEEFVAIGSPALONTVTGIVSTAQREGRELGRDSDMDYIQTDAIINYNGSGP 189
DB 272 ELRPEEFVAIGSPALONTVTGIVSTAQREGRELGRDSDMDYIQTDAIINYNGSGP 331
QY 190 LVNLGEVIGINTLVKTGIFSPALSDRTFLTEFODKQ---WKRRFGIMRTT 246
DB 332 LVNLGEVIGINTLVKTGIFSPALSDRTFLTEFODKQ---WKRRFGIMRTT 391
QY 247 PSVLDELKASNDPFEVSSGIYQVAPNSPQSGIGIDGDIIVKNGRPLVDSSELOEA 306
DB 392 SSKAKELDRHRDPDVGAYIIIEVPTPAAGLAKENDVILISNGSVSANDVSDV 451
QY 307 VLTESPILLEVRGNDLLFSIAPREV 333
DB 452 IKREBTLNMMVVRGNDIMITIVIPETI 478

RESULT 5
US-08-923-454A-8
Sequence 8, Application US/08923454A
Patent No. 6004794
GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Liyi, George
APPLICANT: Kairan, Eric
APPLICANT: Clinkenbeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-923-454A-8

Query Match 52.5%; Score 882; DB 2; Length 458;
Best Local Similarity 52.5%; Pred. No. 3.1e-86;
Matches 169; Conservative 72; Mismatches 71; Indels 10; Gaps 2;

QY 15 SSPRYKFNFIADVVEKIAPAVNHLEFLRHPLEFGNVPPLSSGSGFIMSEAGLIITNAHV 74
DB 141 ASPRQVNFYFIADVVEKIAPAVNHLEFLRHPLEFGREVPVSSGSGFVVAADGLIVTNAHV 200
QY 75 SNSAPARQOLKVQLONGDSYEATIKDIDKSDIATIKIHPKKLPVLLGHSADLRG 134
DB 201 AD-----RRRVRELKNGATYEAKIKDVEKADIALIKIDHCKLPVLLGHSADLRG 254
QY 135 EFVVAIGSPALONTVTGIVSTAQREGRELGRDSDMDYIQTDAIINYNGSGPVLNLD 194
DB 255 EFVVAIGSPALONTVTGIVSTAQREGRELGRDSDMDYIQTDAIINYNGSGPVLNLD 314
QY 195 GEVIGINTLVKTGIFSPALSDRTFLTEFODKQ---IKWKRRFGIMRTTSPSLV 250
DB 315 GEVIGINTLVKTGIFSPALSDRTFLTEFODKQ---IKWKRRFGIMRTTSPSLV 374
QY 251 DELKASNDPFEVSSGIYQVAPNSPQSGIGIDGDIIVKNGRPLVDSSELOEAUTE 310
DB 375 AELQREPSFPDVGAYIIIEVPTPAAGLAKENDVILISNGSVSANDVSDV 434
QY 311 SPILLEVRGNDLLFSIAPREV 332
DB 435 SOLAVQIRKRETLTVYTPREV 456

RESULT 6
US-08-923-454A-25
Sequence 25, Application US/08923454A
Patent No. 6004794
GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Liyi, George
APPLICANT: Kairan, Eric
APPLICANT: Clinkenbeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
US-08-923-454A-25
```

```
Query Match 52.5%; Score 882; DB 2; Length 458;
Best Local Similarity 52.5%; Pred. No. 3,1e-86;
Matches 169; Conservative 72; Mismatches 71; Indels 10; Gaps 2;

QY 15 SSPPRYKFNFIADVVEKIAPAVNHIEFLRHPLEGRNVPLSSGSGFIMSEAGLIITNAHV 74
DB 141 ASPRSQYNFIADVVEKIAPAVNHIEFLRHPLEGRNVPLSSGSGFIMSEAGLIITNAHV 200
QY 75 SSNSAAPGRQOLKVQLONGSDYEATIKDIDKSDIATIKIHPKKLPLVLLGHSADLRPG 134
DB 201 AD-----RRRVRLSLSGDTYEAVNVAVDPVADIALIRIQTKERPLPLPGRSADVROG 254
QY 135 EFVVAIGSPFALONTTGTIVSTAOEGREGLGRDSMDIYQTDALINNGSGPLVND 194
DB 255 EFVVAIGSPFALONTTGTIVSTAOEGREGLGRDSMDIYQTDALINNGSGPLVND 314
QY 195 GEVIGINTKVTAGISFAIPSDRITRFLTEFQDKQ----IKDWKRRFIGIRMTITPSLV 250
DB 315 GEVIGINTKVTAGISFAIPSDRITRFLTEFQDKQ----IKDWKRRFIGIRMTITPSLV 374
QY 251 DELKASNDPPEVSSGIYVQEVAPNSPQSGIQQDDIIVKNGRPVDSSELQEAVALTE 310
DB 375 AELQLRSEFPDPDQGHVLIHKVILGSPAHRAGLRPGDVIILAGQWQNAEDYEAVRTQ 434
QY 311 SPLLEVRGNDLLFSTIAPEV 332
DB 435 SOLAVQIRRGRETLLVYTPEV 456
```

```
RESULT 7
US-09-008-271A-11
Sequence 11, Application US/09008271A
Patent No. 6203979
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Hillman, Jennifer L.
Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
```

```
Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
US-09-008-271A-11
```

```
Query Match 52.5%; Score 882; DB 2; Length 458;
Best Local Similarity 52.5%; Pred. No. 3,1e-86;
Matches 169; Conservative 72; Mismatches 71; Indels 10; Gaps 2;

QY 15 SSPPRYKFNFIADVVEKIAPAVNHIEFLRHPLEGRNVPLSSGSGFIMSEAGLIITNAHV 74
DB 141 ASPRSQYNFIADVVEKIAPAVNHIEFLRHPLEGRNVPLSSGSGFIMSEAGLIITNAHV 200
QY 75 SSNSAAPGRQOLKVQLONGSDYEATIKDIDKSDIATIKIHPKKLPLVLLGHSADLRPG 134
DB 201 AD-----RRRVRLSLSGDTYEAVNVAVDPVADIALIRIQTKERPLPLPGRSADVROG 254
QY 135 EFVVAIGSPFALONTTGTIVSTAOEGREGLGRDSMDIYQTDALINNGSGPLVND 194
DB 255 EFVVAIGSPFALONTTGTIVSTAOEGREGLGRDSMDIYQTDALINNGSGPLVND 314
QY 195 GEVIGINTKVTAGISFAIPSDRITRFLTEFQDKQ----IKDWKRRFIGIRMTITPSLV 250
DB 315 GEVIGINTKVTAGISFAIPSDRITRFLTEFQDKQ----IKDWKRRFIGIRMTITPSLV 374
QY 251 DELKASNDPPEVSSGIYVQEVAPNSPQSGIQQDDIIVKNGRPVDSSELQEAVALTE 310
DB 375 AELQLRSEFPDPDQGHVLIHKVILGSPAHRAGLRPGDVIILAGQWQNAEDYEAVRTQ 434
QY 311 SPLLEVRGNDLLFSTIAPEV 332
DB 435 SOLAVQIRRGRETLLVYTPEV 456
```

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RESULT 8
US-09-968-415-11
Sequence 11, Application US/09968415
Patent No. 6855811
```

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Db      435 SQLAVQIRGRETLLTVTPREV 456

RESULT 9
US-09-075-460-5
; Sequence 5, Application US/09075460A
; Patent No. 6489136
; GENERAL INFORMATION:
; APPLICANT: ZERTVOB, Antonia S.
; TITLE OF INVENTION: CELL PROLIFERATION RELATED GENES
; FILE REFERENCE: 10284/004001
; CURRENT APPLICATION NUMBER: US/09/075,460A
; CURRENT FILING DATE: 1998-05-08
; EARLIER APPLICATION NUMBER: US 60/446,077
; EARLIER FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 529
; TYPE: PROT
; ORGANISM: Homo sapiens
US-09-075-460-5

Query Match      52.5%; Score 882; DB 2; Length 529;
Best Local Similarity 52.5%; Pred. No. 4e-86;
Matches 169; Conservative 72; Mismatches 71; Indels 10; Gaps 2

Qy      15 SSPPRYKFNFIADVVEKTAIPAVVHIELFLRHP,FGRNVLSSGSGFIMSEAGLIITNAHV 74
      ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      212 ASPRSQVNFIDVVEKTAIPAVVYIEILDRHPFLGREVDISNGSGFVAVADGLITNAHV 271
      ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy      75 SSNSAAPGRQOLKVLQLONGDSYEATKIDDKSDPATIKIRPKKGLPVLLGHSADLRG 134
      ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      272 AD-----RRRVRLRLSGDTYEAVVAVADVDADTATLRIGKEPLPTPLGRSADVRG 325
      ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy      135 EFVAIGSPFLQNTVTGTGIYSTQREGRELGRSDMDYIQTDAIINVGNSGFLVND 194
      ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      326 EFVAWMSGFLQNTITISGIVSSAQRPRADLGLPTNVEYIQTDAIDFGNSGFLVND 385
      ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy      195 GEVIGINTLKTAGISFPAIPSDRITRFLTEFODKQ----IDWKRRFGIGIRMRITTPSLV 250
      ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      386 GEVIGVMTMKTAGISFPAIPSDRLREFLHRBEKKNSSSGISGQRRYIGVMMLTISPIL 445
      ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy      251 DELKASNDPFPEVSSGIYQVAPNPSQRCGIQDGLIIVKNGRPLVDSSELQAVLVE 310
      ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      446 AELQIRESPFDVQHGVLIRKVIILGSPHRRAGLRPGDVILAIIGEQVQNAEDVYEAVRQ 505
      ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy      311 SPILLEVRGRNDLLFSIAPREV 332
      ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      506 SQLAVQIRGRETLLTVTPREV 527

RESULT 10
US-08-923-454A-31
; Sequence 31, Application US/08923454A
; Patent No. 6004794
; GENERAL INFORMATION:
; APPLICANT: Creasy, Caretha
; APPLICANT: Livl, George
; APPLICANT: Kattan, Eric
; APPLICANT: Clinkendeard, Helen
; APPLICANT: Browne, Michael
; APPLICANT: Southan, Christopher
; TITLE OF INVENTION: HUMAN SERINE PROTEASE
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,454A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/025436
; FILING DATE: 06-SEPT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50547
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORIGINAL SOURCE: 24 Xaa = Arg or Cys
; ORIGINAL SOURCE: 278 Xaa = Ala or Val
US-08-923-454A-31

```

```

Query Match      52.3%; Score 878; DB 2; Length 458;
Best Local Similarity 52.2%; Pred. No. 8.5e-86;
Matches 168; Conservative 72; Mismatches 72; Indels 10; Gaps 2;

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QY 15 SSPRYENFADVVEKIAVAVHIEFLRHPFLGRNVPVLSGSGFIMSEAGLITNAHV 74
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 141 ASRSQYNFADVVEKIAVAVHIEFLRHPFLGRNVPVLSGSGFIMSEAGLITNAHV 200
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 75 SSNSAAPGRQQLKVOLOMGDSYEATIKIDKSDIATIKIHPKKLPVLLGHSADLRG 134
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 201 AD-----RRRVAVRLSGDTVEAVVAVADVPVADIVTLRIQTREPLPLIGRSADVRRG 254
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 135 EFVVALGSPALONTTGTGIVTAOREGRELGRDSDMDYIQTDAIINTGNSGGLVND 194
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 255 EFVVALGSPALONTTGTGIVTAOREGRELGRDSDMDYIQTDAIINTGNSGGLVND 314
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 195 GEVIGINTLKVTAIGISPAIPSDRITPLTEFODKQ---IKMKKRFIGIRKRTTPTSLV 250
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 315 GEVIGINTLKVTAIGISPAIPSDRITPLTEFODKQ---IKMKKRFIGIRKRTTPTSLV 374
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 251 DELKASNPDPPEVSSGIYQVQVAPNSPSQSGIQQDGIIVKNGRPLVDSSELOEAVLTE 310
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 375 AELQAREPSFPDVGVLHKLVLGSPARAGLRPGDVLIALGQVQVQAEDEVYAVRQ 434
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 311 SPILLEVRGNDLLFSIAPEV 332
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 435 SOLAVQIRGRGRTLLVTPPEV 456
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

```

```

RESULT 11
US-09-724-864-55
; Sequence 55, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.105001

```

```

; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-55

```

```

Query Match      51.4%; Score 862.5; DB 2; Length 400;
Best Local Similarity 57.2%; Pred. No. 3.2e-84;
Matches 167; Conservative 61; Mismatches 55; Indels 9; Gaps 2;

```

```

QY 45 PLFGNVPVLSGSGFIMSEAGLITNAHVSSNSAAPRQQLKVOLOMGDSYEATIKID 104
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 114 PLTQEIPISSSGSGFVSEDLITVNAHVLTN-----QKIQVELQSGAREATVKID 167
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 105 KSDIATIKIHPKKLPVLLGHSADLRPGEFVVAIGSPALONTTGTGIVTAOREGRE 164
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 168 HRLDALIKIBDTELPLVLLGRSSDLRAGEFVVALGSPFSLQNTVTAIGIVSTTCRGRE 227
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 165 LGLRSDMDYIQTDAIINTGNSGGLVNLDEGVIGINTLKVTAIGISPAIPSDRITPLTE 224
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 228 LGLKNSDIDYIQTDAIINTGNSGGLVNLDEGVIGINTLKVTAIGISPAIPSDRITPLTE 287
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 225 FQDKQIK--DWKKRFIGIRKRTTPTSLVDELKASNPDPPEVSSGIYQVQVAPNSPSQSG 281
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 288 YHERQLKKAAPLQKKYGLGRMLPLTLNLQEWKQDPFPVSSGVFVYEQGSAAS 347
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 282 GIQDGIIVKNGRPLVDSSELOEAVLTPSPLLEVRGNDLLFSIAPEV 333
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 348 GIRDHDIIVSINGQPVTTTVDVTEAVKNDPLSLIIVLGSQTLFLTPPEII 399
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

```

```

RESULT 12
US-08-923-454A-6
; Sequence 6, Application US/08923454A
; Patent No. 6004794
; GENERAL INFORMATION:
; APPLICANT: Creasy, Caretha
; APPLICANT: Lavi, George
; APPLICANT: Kattan, Eric
; APPLICANT: Clinkbeard, Helen
; APPLICANT: Browne, Michael
; APPLICANT: Southan, Christopher
; TITLE OF INVENTION: HUMAN SERINE PROTEASE
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,454A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/025436
; FILING DATE: 06-SEPT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50547

```



```

1 TELECOMMUNICATION INFORMATION
2
3 TELEPHONE: 610-270-5096
4
5 TELEFAX: 610-270-5090
6
7 TEXT:
8
9 INFORMATION FOR SEQ ID NO: 6:
10
11 SEQUENCE CHARACTERISTICS:
12
13 LENGTH: 423 amino acids
14
15 TYPE: amino acid
16
17 STRANDEDNESS: single
18
19 TOPOLOGY: linear
20
21 MOLECULE TYPE: peptide
22
23 HYPOTHEetical: NO
24
25 ANTI-SENSE: NO
26
27 PAYMENT TYPE: N-terminal
28
29 ORIGINAL SOURCE:
30
31 US-08-923-454A-6

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Query Match	46.4%	Score 779	DB 2:	Length 423
Best Local Similarity	47.6%	Pred	No. 3.7e-75	
Matches 158	Conservative 64	Mismatches 58	Indels 52	Gaps 4

Qy	15	SSPRKFNPIADVVKIMPAVVHLELHPLEGRAVPLSSGSGFLTSEKGLITTAHV	74
Db	128	ASPRQYNFIDWVEKTAPAVVYIELDHPPLGRVRPISNSGSFFVAADGLVTNAHV	197
Qy	75	SSNSAAPROOLKVOLONGDSYEATIKDIDKSDIATIYKHKKKLTVLLGHSAULRPG	134
Db	188	AD-----RRRVKVLISGDITEAVVTAVDPAVDITLTLETQTEPEPLPLEGSAVDRQG	241
Qy	135	EFVVAIGSPFALONVTGTIGIVSTAOREGREGLRUSDMDYIQTDALINYNSGGPLVNT-	193
Db	242	EFVAMGSPFALQNITTSIGIVSASRAPRDGLPQINVERIQTDAIDPNSGSLPVNLA	301
Qy	194	-----DGEVIGINTLKTAGISFALPSDRITRELFTEPDQK--IKMKKKEFIGI	240
Db	302	RELGAVSLQDDGEVIGINTTKVTAGISFALPSRLREFLRHEKKNSSSGSIGSRRYTGV	361
Qy	241	RMRITTBVLDELKASNPDFEEVSSGITVQEVAVNSPSORGIGQQDGDIYKNGRPVLVS	300
Db	362	MMLTISP-----RAGIRPDGVILAIIEQWAVONA	389
Qy	301	SLEQAVLTESPILLEVRGNDDLFSIAPEV	332
Db	390	EDVEAVRTQSGLAVOIRRGRETLLTYLPVE	421

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1  RESULT 13
2  US-08-923-454A-29
3  Sequence 29, Application US/08923454A
4  Patent No. 6004794
5  GENERAL INFORMATION:
6  APPLICANT: Creasy, Caretha
7  APPLICANT: Livi, George
8  APPLICANT: Karan, Eric
9  APPLICANT: Clinkenbeard, Helen
10 APPLICANT: Browne, Michael
11 APPLICANT: Southan, Christopher
12 TITLE OF INVENTION: HUMAN SERINE PROTEASE
13 NUMBER OF SEQUENCES: 40
14 CORRESPONDENCE ADDRESS:
15 ADDRESSEE: SmithKline Beecham Corporation
16 STREET: 709 Swedeland Road
17 CITY: King of Prussia
18 STATE: PA
19 COUNTRY: USA
20 ZIP: 19406
21 COMPUTER READABLE FORM:
22 MEDIUM TYPE: Diskette
23 COMPUTER: IBM Compatible
24 OPERATING SYSTEM: DOS
25 SOFTWARE: FastSeq Version 1.5
26 CURRENT APPLICATION DATA:
27 APPLICATION NUMBER: US/08/923,454A

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```

1      FILING DATE:
2      CLASSIFICATION: 435
3      PRIOR APPLICATION DATA:
4      APPLICATION NUMBER: 60/025436
5      FILING DATE: 06-SEP-1996
6      ATTORNEY/AGENT INFORMATION:
7      NAME: Baumeister, Kirk
8      REGISTRATION NUMBER: 33,833
9      REFERENCE/DOCKET NUMBER: P50547
10     TELECOMMUNICATION INFORMATION:
11     TELEPHONE: 610-270-5096
12     TELEFAX: 610-270-5090
13     TELEX:
14     INFORMATION FOR SEQ ID NO: 29:
15     SEQUENCE CHARACTERISTICS:
16     LENGTH: 436 amino acids
17     TYPE: amino acid
18     STRANDEDNESS: single
19     TOPOLOGY: linear
20     MOLECULE TYPE: protein
21     HYPOTHETICAL: NO
22     ANTI-SENSE: NO
23     FRAGMENT TYPE: internal
24     ORIGINAL SOURCE:
25     OS-08-923-454A-29

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Query Match	46.4%;	Score 779;	DB 2;	Length 436;
Best Local Similarity	47.6%;	Pred. No. 3.8e-75;		
Matches 158;	Conservative 64;	Mismatches 58;	Indels 52;	Gaps 4

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Qy 15 SGRKXENIADUWEEKIAPAVVHIELFRLHPLFRBNVPLSSGSGFISSEAGLITTAHV 74
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 141 ASRSQYNFIADUWEEKIAPAVVYIELDRHPLFRREVPLISNGSFVVAAGLIVTAAHV 200
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 75 SSSMAAPGQOLKQYOLONGDSEYATIKOIDDKSUIATIKIHPKKGLPVLLIGHSADLRPG 134
   AD-----RRRRVAVLLSGDTIEAVVTAVDVPAIATLRITQTEHPLTTLPLGMSADVROG 254
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 201 AD-----RRRRVAVLLSGDTIEAVVTAVDVPAIATLRITQTEHPLTTLPLGMSADVROG 254
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 135 EFVVAIGSFPAIONVTVTGIVSTAQREGREGLDSDMDYIQTDAIINYNGSGPLVNL- 193
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 255 EFVVAIGSFPAIONVTITSGIVSSAQRPARDGLQGTWVEYIQTDAIDFNSGSGPLVNL4 314
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 194 -----DGEVIGINTLKVTAIGISFPAISDRITRFLTEFPQKQ-----IKDKKKPFIGI 240
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 315 RELGAVSLDGEVIGINTVMKTATAGISFPAISDRILREFLHGEKKNSSGSISGQRRIYGV 374
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 241 KMRITTPSLVDELKASNDPPEVSVSGIYQGVAVPANSQSGKIODGIIYKVNKGRPLVDS 300
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 375 MMLTLP-----RAGLRPGVIAIIGEQWVONA 402
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 301 SELQEAUVTLPFLLEVRGNDLLFLSTAPEV 332
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 403 EDVTEAVRTQSGLAVOIRRGRETTLLVYTPPV 434
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

```

US-087 14
US-087-923-454A-4
Sequence 4, Application US/08923454A
Patent No. 6004794
GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Livi, George
APPLICANT: Karran, Eric
APPLICANT: Clinkenbeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESS: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA

COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33, 833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-923-454A-4

Query Match 33.6%; Score 564; DB 2; Length 323;
Best Local Similarity 59.9%; Pred. No. 3.9e-52;
Matches 109; Conservative 37; Mismatches 30; Indels 6; Gaps 1;
QY 15 SSRRYKFNFIADYVEKIAPAVVHIELFLRHPLFGNNVPLSSGGGFIMSEAGLIITNAHV 74
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
DB 87 ASRRSQYNFIADYVEKTAAPAVVYIELIDRHPLFGREVPISNGSGFVAADGLIVTNAHV 146
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
QY 75 SSNSAAPGRQOLKVLQNGDSYEATIKDKKSDIATIKHPKKLPVLLIGHSADLRPG 134
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
DB 147 AD-----RRRVRLISGDTYEAVTAVDPVADITLRIQTKEPLPTPLGRSADVROG 200
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
QY 135 EFVVAIGSPFALQNTVTGIVSTAQREGRELGLRDSMDYIQTDAIINYNGSGPLVND 194
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
DB 201 EFVVAIGSPFALQNTITSGIVSSAQRPARDLGLPQTNVEYIQTDAIDFGNSGGLVNLV 260
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
QY 195 GE 196
|
DB 261 SE 262

RESULT 15
US-08-923-454A-27
Sequence 27, Application US/08923454A
GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Lavi, George
APPLICANT: Kattan, Eric
APPLICANT: Clinkenbeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSES: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia

STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33, 833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-923-454A-27

Query Match 33.6%; Score 564; DB 2; Length 377;
Best Local Similarity 59.9%; Pred. No. 5e-52;
Matches 109; Conservative 37; Mismatches 30; Indels 6; Gaps 1;
QY 15 SSRRYKFNFIADYVEKIAPAVVHIELFLRHPLFGNNVPLSSGGGFIMSEAGLIITNAHV 74
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
DB 141 ASRRSQYNFIADYVEKTAAPAVVYIELIDRHPLFGREVPISNGSGFVAADGLIVTNAHV 200
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
QY 75 SSNSAAPGRQOLKVLQNGDSYEATIKDKKSDIATIKHPKKLPVLLIGHSADLRPG 134
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
DB 201 AD-----RRRVRLISGDTYEAVTAVDPVADITLRIQTKEPLPTPLGRSADVROG 254
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
QY 135 EFVVAIGSPFALQNTVTGIVSTAQREGRELGLRDSMDYIQTDAIINYNGSGPLVND 194
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
DB 255 EFVVAIGSPFALQNTITSGIVSSAQRPARDLGLPQTNVEYIQTDAIDFGNSGGLVNLV 314
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
QY 195 GE 196
|
DB 315 SE 316

Search completed: February 21, 2006, 21:03:03
Job time : 48 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2006, 21:13:11 : Search time 163 Seconds
(without alignments)
856.166 Million cell updates/sec

Title: US-10-617-443B-2

Perfect score: 1679
Sequence: 1 MHIALPASAGLHQLSSPRK.....LEVARGNDLLFSTAPEVVM 334

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBSCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBSCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBSCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10_PUBSCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBSCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBSCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1679	100.0	334	4 US-10-189-099A-2	Sequence 2, Appl1
2	1679	100.0	334	5 US-10-617-443B-2	Sequence 2, Appl1
3	1635	97.4	348	3 US-09-796-753-34	Sequence 34, Appl1
4	1635	97.4	453	3 US-09-796-753-32	Sequence 32, Appl1
5	1635	97.4	453	4 US-10-275-505-14	Sequence 14, Appl1
6	1635	97.4	453	4 US-10-381-820A-8	Sequence 8, Appl1
7	1635	97.4	453	5 US-10-485-313A-33	Sequence 33, Appl1
8	1635	97.4	453	5 US-11-140-224-14	Sequence 14, Appl1
9	1536	91.5	459	5 US-10-485-313A-27	Sequence 27, Appl1
10	1378	82.1	286	3 US-09-764-898-256	Sequence 256, App
11	1353.5	80.6	452	4 US-10-301-822-79	Sequence 79, Appl1
12	1117	66.5	357	3 US-10-485-313A-34	Sequence 34, Appl1
13	1105	65.8	330	3 US-09-764-898-184	Sequence 184, App
14	1057	63.0	363	5 US-10-485-313A-39	Sequence 39, Appl1
15	1034.5	61.6	447	4 US-10-104-047-2765	Sequence 2765, App
16	1034.5	61.6	480	4 US-10-170-385-355	Sequence 355, App
17	1034.5	61.6	480	4 US-10-772-636-48	Sequence 48, Appl1
18	1027.5	61.2	517	4 US-10-264-049-2310	Sequence 2310, App
19	994.5	59.2	405	3 US-09-925-298-552	Sequence 552, App
20	994.5	59.2	405	4 US-10-102-806-552	Sequence 552, App
21	890	53.0	476	3 US-09-935-390A-37	Sequence 37, Appl1
22	890	53.0	476	4 US-10-789-241-50	Sequence 50, Appl1
23	890	53.0	476	5 US-10-772-636-8	Sequence 8, Appl1
24	882	52.5	321	4 US-10-730-476A-52	Sequence 52, Appl1
25	882	52.5	321	5 US-10-730-476A-52	Sequence 52, Appl1
26	882	52.5	325	4 US-10-730-476A-44	Sequence 44, Appl1
27	882	52.5	325	5 US-10-730-476A-44	Sequence 44, Appl1

28	882	52.5	458	3 US-09-968-415-11	Sequence 11, Appl1
29	882	52.5	458	4 US-10-197-634-1	Sequence 1, Appl1
30	882	52.5	458	4 US-10-180-719-11	Sequence 11, Appl1
31	882	52.5	458	4 US-10-352-684A-10	Sequence 10, Appl1
32	882	52.5	458	6 US-11-045-577-11	Sequence 11, Appl1
33	882	52.5	529	4 US-10-216-667-5	Sequence 5, Appl1
34	862	51.3	325	4 US-10-730-476A-45	Sequence 45, Appl1
35	862	51.3	325	4 US-10-730-476A-46	Sequence 46, Appl1
36	862	51.3	325	4 US-10-730-476A-47	Sequence 47, Appl1
37	862	51.3	325	4 US-10-730-476A-53	Sequence 53, Appl1
38	862	51.3	325	5 US-10-730-476A-45	Sequence 45, Appl1
39	862	51.3	325	5 US-10-730-476A-46	Sequence 46, Appl1
40	862	51.3	325	5 US-10-730-476A-47	Sequence 47, Appl1
41	862	51.3	325	5 US-10-730-476A-53	Sequence 53, Appl1
42	854	50.9	178	3 US-09-969-384-18	Sequence 18, Appl1
43	689	41.0	221	4 US-10-730-476A-54	Sequence 54, Appl1
44	689	41.0	221	5 US-10-730-476A-54	Sequence 54, Appl1
45	689	41.0	225	4 US-10-730-476A-48	Sequence 48, Appl1

ALIGNMENTS

RESULT 1
US-10-189-099A-2
; Sequence 2, Application US/10189099A
; Publication No. US20040005659A1
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew L
; APPLICANT: Qi, Jian-shen
; APPLICANT: Chen, Caifan
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OR INVENTION: Human PRSS-11 like S2 serine protease and uses thereof
; FILE REFERENCE: ORI-1644
; CURRENT APPLICATION NUMBER: US/10/189, 099A
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-189-099A-2

Query Match	100.0%	Score 1679	DB 4	Length 334
Best Local Similarity	100.0%	Pred. No. 4.5e-144		
Matches 334	Conservative	0	Mismatches	0
			Indels	0
			Gaps	0
QY	1	MHIALPASAGLHQLSSPRKFNFIADVVEKIAPAVHIEFLRHPVPLSSGSGFI	60	
DB	1	MHIALPASAGLHQLSSPRKFNFIADVVEKIAPAVHIEFLRHPVPLSSGSGFI	60	
QY	61	MSEAGLIITNNAHVSSNSAPRQQLKVQLONGDSYEATIKDIDKSDIATIKHPKKKL	120	
DB	61	MSEAGLIITNNAHVSSNSAPRQQLKVQLONGDSYEATIKDIDKSDIATIKHPKKKL	120	
QY	121	PVLLIGHADLRPGFFVVAIGSPFALQNTVTGISTVQREKREGLDSDMDVYQTAI	180	
DB	121	PVLLIGHADLRPGFFVVAIGSPFALQNTVTGISTVQREKREGLDSDMDVYQTAI	180	
QY	181	INVGSGPLVNLDEVGINTLKTAGISPAIPSDRITRFLTEPQDQIKDKKRFICI	240	
DB	181	INVGSGPLVNLDEVGINTLKTAGISPAIPSDRITRFLTEPQDQIKDKKRFICI	240	
QY	241	RNRITTPSLVDELKASNDPPEVSSGIYQVAVPNSPQKGIQDGIIVKXNGRPLVDS	300	
DB	241	RNRITTPSLVDELKASNDPPEVSSGIYQVAVPNSPQKGIQDGIIVKXNGRPLVDS	300	
QY	301	SELQAVVLTESPLLEVRGNDLLFSTAPEVVM	334	
DB	301	SELQAVVLTESPLLEVRGNDLLFSTAPEVVM	334	

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RESULT 2
US-10-617-443B-2
; Sequence 2, Application US/10617443B
; Publication No. US20050019777A1
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew L
; APPLICANT: Qi, Jian-shen
; APPLICANT: Chen, Caillin
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Human PRSS-11 like S2 serine protease and uses thereof
; FILE REFERENCE: ORT-1644
; CURRENT APPLICATION NUMBER: US/10/617,443B
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-617-443B-2

Query Match          100.0%; Score 1679; DB 5; Length 334;
Best Local Similarity 100.0%; Pred. No. 4, Se-144;
Matches 334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHIALPASAGLHQLSSPRYKFNFIADVVEKIAPAVVHIELFLRHPFGFGRVPLSSGSGFT 60
DB 1 MHIALPASAGLHQLSSPRYKFNFIADVVEKIAPAVVHIELFLRHPFGFGRVPLSSGSGFT 60
QY 61 MSAAGLIITNAHVSSNSAAPGRQQLKVQLQNGDSYEATIKDIDKSDIATIKIHPKKKL 120
DB 61 MSAAGLIITNAHVSSNSAAPGRQQLKVQLQNGDSYEATIKDIDKSDIATIKIHPKKKL 120
QY 121 PVLILGHSADLRGEFVVAIGSPFALONTTGTIVSTAOREGSELGRSDMDYIOTDAI 180
DB 121 PVLILGHSADLRGEFVVAIGSPFALONTTGTIVSTAOREGSELGRSDMDYIOTDAI 180
QY 181 INYNGSGPLVNDGEVIGINTLKTAGISFAIPSDRITFLTEFODKOIKMKKRFIFI 240
DB 181 INYNGSGPLVNDGEVIGINTLKTAGISFAIPSDRITFLTEFODKOIKMKKRFIFI 240
QY 241 RMRITPSLVDELKASNPDPPEVSSGIYVOEVAPNSPSQGGIQQDDIIYKVGRLVDS 300
DB 241 RMRITPSLVDELKASNPDPPEVSSGIYVOEVAPNSPSQGGIQQDDIIYKVGRLVDS 300
QY 301 SELQEAULTESPILLLEVRGNDLPLFSIAPEVVM 334
DB 301 SELQEAULTESPILLLEVRGNDLPLFSIAPEVVM 334

RESULT 3
US-09-796-753-34
; Sequence 34, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
```

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; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 34
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Mouse
US-09-796-753-34

Query Match          97.4%; Score 1635; DB 3; Length 348;
Best Local Similarity 100.0%; Pred. No. 4, Se-140;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GLHQLSSPRYKFNFIADVVEKIAPAVVHIELFLRHPFGFGRVPLSSGSGFTMSEAGLIIT 69
DB 24 GLHQLSSPRYKFNFIADVVEKIAPAVVHIELFLRHPFGFGRVPLSSGSGFTMSEAGLIIT 83
QY 70 NAHVSSNSAAPGRQQLKVQLQNGDSYEATIKDIDKSDIATIKIHPKKKL PVLILGSHA 129
DB 84 NAHVSSNSAAPGRQQLKVQLQNGDSYEATIKDIDKSDIATIKIHPKKKL PVLILGSHA 143
QY 130 DLRRGEFVVAIGSPFALONTTGTIVSTAOREGSELGRSDMDYIOTDAI INYNGSGP 189
DB 144 DLRRGEFVVAIGSPFALONTTGTIVSTAOREGSELGRSDMDYIOTDAI INYNGSGP 203
QY 190 LVNLDGEVIGINTLKTAGISFAIPSDRITFLTEFODKOIKMKKRFI GRMRTTIPSL 249
DB 204 LVNLDGEVIGINTLKTAGISFAIPSDRITFLTEFODKOIKMKKRFI GRMRTTIPSL 263
QY 250 VDELKASNPDPPEVSSGIYVOEVAPNSPSQGGIQQDDIIYKVGRLVDSSELQEAULT 309
DB 264 VDELKASNPDPPEVSSGIYVOEVAPNSPSQGGIQQDDIIYKVGRLVDSSELQEAULT 323
QY 310 ESPILLLEVRGNDLPLFSIAPEVVM 334
DB 324 ESPILLLEVRGNDLPLFSIAPEVVM 348
```

RESULT 4
US-09-796-753-32; Sequence 32, Application US/09796753
; Publication No. US20030027998A1

GENERAL INFORMATION:

; APPLICANT: McCarthy, Sean A.

; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF

; FILE REFERENCE: 7853-227-999

; CURRENT APPLICATION NUMBER: US/09/796,753

; CURRENT FILING DATE: 2001-03-01

; PRIOR APPLICATION NUMBER: 09/183,175

; PRIOR FILING DATE: 1998-10-30

; PRIOR APPLICATION NUMBER: 09/223,094

; PRIOR FILING DATE: 1998-12-30

; PRIOR APPLICATION NUMBER: 09/223,546

; PRIOR FILING DATE: 1998-12-30

; PRIOR APPLICATION NUMBER: 09/224,246

; PRIOR FILING DATE: 1998-12-30

; PRIOR APPLICATION NUMBER: 09/259,388

; PRIOR FILING DATE: 1999-02-26

; PRIOR APPLICATION NUMBER: 60/122,458

; PRIOR FILING DATE: 1999-03-01

; PRIOR APPLICATION NUMBER: 09/312,359

; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: 09/336,536

; PRIOR FILING DATE: 1999-06-18

; PRIOR APPLICATION NUMBER: 09/342,687

; PRIOR FILING DATE: 1999-06-29

; PRIOR APPLICATION NUMBER: 09/345,464

; PRIOR FILING DATE: 1999-06-30

; PRIOR APPLICATION NUMBER: 09/365,164

; PRIOR FILING DATE: 1999-07-30

; PRIOR APPLICATION NUMBER: 09/399,723

; PRIOR FILING DATE: 1999-09-20

; PRIOR APPLICATION NUMBER: 09/409,634

; PRIOR FILING DATE: 1999-09-30

; PRIOR APPLICATION NUMBER: 09/471,179

; PRIOR FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: 09/474,071

; PRIOR FILING DATE: 1999-12-29

; PRIOR APPLICATION NUMBER: 09/474,072

; PRIOR FILING DATE: 1999-12-29

; PRIOR APPLICATION NUMBER: 09/514,010

; PRIOR FILING DATE: 2000-02-25

; PRIOR APPLICATION NUMBER: 09/516,745

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: 09/572,002

; PRIOR FILING DATE: 2000-05-14

; PRIOR APPLICATION NUMBER: 09/597,993

; PRIOR FILING DATE: 2000-06-19

; PRIOR APPLICATION NUMBER: 09/599,596

; PRIOR FILING DATE: 2000-06-22

; PRIOR APPLICATION NUMBER: 09/630,334

; PRIOR FILING DATE: 2000-07-31

; PRIOR APPLICATION NUMBER: 09/606,565

; PRIOR FILING DATE: 2000-06-29

; PRIOR APPLICATION NUMBER: 09/606,317

; PRIOR FILING DATE: 2000-06-29

; PRIOR APPLICATION NUMBER: 09/665,666

; PRIOR FILING DATE: 2000-09-20

; PRIOR APPLICATION NUMBER: 09/677,751

; PRIOR FILING DATE: 2000-09-30

; NUMBER OF SEQ ID NOS: 162

; SEQ ID NO 32

; LENGTH: 453

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-796-753-32

Query Match 97.4%; Score 1635; DB 3; Length 453;

Best Local Similarity 100.0%; Pred. No. 7.1e-140;

Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GHHQSSRRYKFNPAADVVEKIAPAVNHLEFLRHPLEGRVPLSSGGGFTMSEAGLIT 69
DB 129 GHQSSRRYKFNPAADVVEKIAPAVNHLEFLRHPLEGRVPLSSGGGFTMSEAGLIT 188
QY 70 NAHVSSNSAAPGRQQLKVQKONGDSYEATIKDKDSIDITIKHPKKLPVLLGSHA 129
DB 189 NAHVSSNSAAPGRQQLKVQKONGDSYEATIKDKDSIDITIKHPKKLPVLLGSHA 248
QY 130 DLRPGEFVVAIGSPALQNTVTGIVSTAQREGRELGRSDMDVYIQTDALINYNSSGP 189
DB 249 DLRPGEFVVAIGSPALQNTVTGIVSTAQREGRELGRSDMDVYIQTDALINYNSSGP 308
QY 190 LVNLDEYVIGINTLKTNTGIFSPALPSDITFLTFEPQKQIKDWKREIGIRMTITPSL 249
DB 309 LVNLDEYVIGINTLKTNTGIFSPALPSDITFLTFEPQKQIKDWKREIGIRMTITPSL 368
QY 250 VDELKASNPDPPEVSSGIYQEVAPNSPQSGIQQDGIYKVNGRPLVDSSELQEAVAL 309
DB 369 VDELKASNPDPPEVSSGIYQEVAPNSPQSGIQQDGIYKVNGRPLVDSSELQEAVAL 428
QY 310 ESPLLLEVRGNDLLFSGIAPEVVM 334
DB 429 ESPLLLEVRGNDLLFSGIAPEVVM 453

RESULT 5

US-10-275-505-14

; Sequence 14, Application US/10275505

; Publication No. US20040081961A1

GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: DELEGEAN, Angelo M.; LAL, Preeti G.

; APPLICANT: HAFALIA, April J.A.; PATTERSON, Chandra

; APPLICANT: WALIA, Nardine K.; KEARNEY, Liam

; APPLICANT: TRIBOULEY, Catherine M.; KHAN, Farrah A.

; APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.

; APPLICANT: AZIMZAI, Yalda; ELIOTY, Vicki S.

; APPLICANT: NGUYEN, Danielle B.; GANDHI, Ameena R.

; APPLICANT: YANG, Junming; HERNANDEZ, Roberto

; APPLICANT: POLICKY, Jennifer L.; LU, Dyung Anna M.

; APPLICANT: REDDY, Roopa M.; YUE, Henry

; APPLICANT: TANG, Y. Tom

; TITLE OF INVENTION: PROTEASES

; FILE REFERENCE: PI-0085 USN

; CURRENT APPLICATION NUMBER: US/10/275,505

; CURRENT FILING DATE: 2002-11-04

; PRIOR APPLICATION NUMBER: PCT/US01/14651

; PRIOR FILING DATE: 2001-05-04

; PRIOR APPLICATION NUMBER: 60/209,402

; PRIOR FILING DATE: 2000-06-01

; PRIOR APPLICATION NUMBER: 60/207,477

; PRIOR FILING DATE: 2000-05-25

; PRIOR APPLICATION NUMBER: 60/205,803

; PRIOR FILING DATE: 2000-05-17

; PRIOR APPLICATION NUMBER: 60/203,566

; PRIOR FILING DATE: 2000-05-11

; PRIOR APPLICATION NUMBER: 60/202,082

; PRIOR FILING DATE: 2000-05-04

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PERL Program

; SEQ ID NO 14

; LENGTH: 453

; TYPE: PRT

; ORGANISM: Homo sapiens

; NAME/KEY: misc.feature

; OTHER INFORMATION: Incyte ID No: 7474343CD1

; US-10-275-505-14

Query Match 97.4%; Score 1635; DB 4; Length 453;

Best Local Similarity 100.0%; Pred. No. 7.1e-140;

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Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 GHHQSSPRYKFNFIADVVEKIAPAVYHIELFLRHPFLGRNVPPLSSGSGFIMSEAGLIT 69
DB 129 GHHQSSPRYKFNFIADVVEKIAPAVYHIELFLRHPFLGRNVPPLSSGSGFIMSEAGLIT 188
QY 70 NAHVSSNSAAPGRQOLKVQLONGDSYEATIKDIDKSDIATIKIHPKKLPVLLGHSA 129
DB 189 NAHVSSNSAAPGRQOLKVQLONGDSYEATIKDIDKSDIATIKIHPKKLPVLLGHSA 248
QY 130 DLAPGEFVVAIGSPFALQNTVTGIVSTAQREGRELGLRSDMDYIQTDAIINYGNSGCP 189
DB 249 DLAPGEFVVAIGSPFALQNTVTGIVSTAQREGRELGLRSDMDYIQTDAIINYGNSGCP 308
QY 190 LVNLDEVGINTLKTATAGISPAIPSDRITRFLTEFODKOIKDKKRFIGIRMTTIPS 249
DB 309 LVNLDEVGINTLKTATAGISPAIPSDRITRFLTEFODKOIKDKKRFIGIRMTTIPS 368
QY 250 VDELKASNPDPPEVSSGIYVOEVAAPNSPQSGGIQDGDIIYKVGSRPLVDSSELQEAVALT 309
DB 369 VDELKASNPDPPEVSSGIYVOEVAAPNSPQSGGIQDGDIIYKVGSRPLVDSSELQEAVALT 428
QY 310 ESPLLEVRNGNDLLFSIAPEVVM 334
DB 429 ESPLLEVRNGNDLLFSIAPEVVM 453

RESULT 6
US-10-381-820A-8
; Sequence 8, Application US/10381820A
; Publication No. US20040142333A1
; GENERAL INFORMATION:
; APPLICANT: Deehun, Lu
; APPLICANT: Song, Ho Yeong
; APPLICANT: Su, Eric Wen
; APPLICANT: Wang, He
; TITLE OF INVENTION: Novel Secreted Proteins and Their Uses
; FILE REFERENCE: X-13974
; CURRENT APPLICATION NUMBER: US/10/381,820A
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-381-820A-8

Query Match 97.4%; Score 1635; DB 4; Length 453;
Best Local Similarity 100.0%; Pred. No. 7.1e-140;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 GHHQSSPRYKFNFIADVVEKIAPAVYHIELFLRHPFLGRNVPPLSSGSGFIMSEAGLIT 69
DB 129 GHHQSSPRYKFNFIADVVEKIAPAVYHIELFLRHPFLGRNVPPLSSGSGFIMSEAGLIT 188
QY 70 NAHVSSNSAAPGRQOLKVQLONGDSYEATIKDIDKSDIATIKIHPKKLPVLLGHSA 129
DB 189 NAHVSSNSAAPGRQOLKVQLONGDSYEATIKDIDKSDIATIKIHPKKLPVLLGHSA 248
QY 130 DLAPGEFVVAIGSPFALQNTVTGIVSTAQREGRELGLRSDMDYIQTDAIINYGNSGCP 189
DB 249 DLAPGEFVVAIGSPFALQNTVTGIVSTAQREGRELGLRSDMDYIQTDAIINYGNSGCP 308
QY 190 LVNLDEVGINTLKTATAGISPAIPSDRITRFLTEFODKOIKDKKRFIGIRMTTIPS 249
DB 309 LVNLDEVGINTLKTATAGISPAIPSDRITRFLTEFODKOIKDKKRFIGIRMTTIPS 368
QY 250 VDELKASNPDPPEVSSGIYVOEVAAPNSPQSGGIQDGDIIYKVGSRPLVDSSELQEAVALT 309
DB 369 VDELKASNPDPPEVSSGIYVOEVAAPNSPQSGGIQDGDIIYKVGSRPLVDSSELQEAVALT 428
QY 310 ESPLLEVRNGNDLLFSIAPEVVM 334
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DB 429 ESPLLEVRNGNDLLFSIAPEVVM 453

RESULT 7
US-10-485-313A-33
; Sequence 33, Application US/10485313A
; Publication No. US20050059002A1
; GENERAL INFORMATION:
; APPLICANT: NIE, Guiying
; APPLICANT: SALMONSEN, Lois Adrienne
; APPLICANT: Li, Ying
; APPLICANT: HAMPTON, Anne Lorraine
; APPLICANT: FINDLAY, John Kerr
; TITLE OF INVENTION: Novel Serine Protease
; FILE REFERENCE: 31633-200357
; CURRENT APPLICATION NUMBER: US/10/485,313A
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: PCT/AU02/01010
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: PR6707
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 453
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-485-313A-33

Query Match 97.4%; Score 1635; DB 5; Length 453;
Best Local Similarity 100.0%; Pred. No. 7.1e-140;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 GHHQSSPRYKFNFIADVVEKIAPAVYHIELFLRHPFLGRNVPPLSSGSGFIMSEAGLIT 69
DB 129 GHHQSSPRYKFNFIADVVEKIAPAVYHIELFLRHPFLGRNVPPLSSGSGFIMSEAGLIT 188
QY 70 NAHVSSNSAAPGRQOLKVQLONGDSYEATIKDIDKSDIATIKIHPKKLPVLLGHSA 129
DB 189 NAHVSSNSAAPGRQOLKVQLONGDSYEATIKDIDKSDIATIKIHPKKLPVLLGHSA 248
QY 130 DLAPGEFVVAIGSPFALQNTVTGIVSTAQREGRELGLRSDMDYIQTDAIINYGNSGCP 189
DB 249 DLAPGEFVVAIGSPFALQNTVTGIVSTAQREGRELGLRSDMDYIQTDAIINYGNSGCP 308
QY 190 LVNLDEVGINTLKTATAGISPAIPSDRITRFLTEFODKOIKDKKRFIGIRMTTIPS 249
DB 309 LVNLDEVGINTLKTATAGISPAIPSDRITRFLTEFODKOIKDKKRFIGIRMTTIPS 368
QY 250 VDELKASNPDPPEVSSGIYVOEVAAPNSPQSGGIQDGDIIYKVGSRPLVDSSELQEAVALT 309
DB 369 VDELKASNPDPPEVSSGIYVOEVAAPNSPQSGGIQDGDIIYKVGSRPLVDSSELQEAVALT 428
QY 310 ESPLLEVRNGNDLLFSIAPEVVM 334
DB 429 ESPLLEVRNGNDLLFSIAPEVVM 453

RESULT 8
US-11-140-224-14
; Sequence 14, Application US/11140224
; Publication No. US20050227280A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DEBEGBANE, Angelo M.; LAL, Preeti G.
; APPLICANT: HAFALIA, April J.A.; PATERSON, Chandra
; APPLICANT: WALIA, Nardinder K.; KEARNNEY, Liam
; APPLICANT: TRIBOULEY, Catherine M.; KHAN, Farrah A.
; APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Yalda; ELLIOTT, Vicki S.
; APPLICANT: NGUYEN, Daniel B.; GANDHI, Ameena R.
; APPLICANT: YANG, Junning; HERNANDEZ, Roberto
```

APPLICANT: POLICKY, Jennifer L.; LU, Dyung Aina M.
APPLICANT: REDDY, Roopa M.; YUE, Henry
APPLICANT: TANG, Y. Tom
TITLE OF INVENTION: PROTEASES
FILE REFERENCE: PI-0085 USN
CURRENT APPLICATION NUMBER: US/11/140,224
CURRENT FILING DATE: 2005-05-31
PRIOR APPLICATION NUMBER: US/10/275,505
PRIOR FILING DATE: 2002-11-04
PRIOR APPLICATION NUMBER: PCT/US01/14651
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/209,402
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: 60/207,477
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/205,803
PRIOR FILING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: 60/203,566
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 60/202,082
PRIOR FILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PERL Program
SEQ ID NO 14
LENGTH: 453
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 7474343CD1
US-11-140-224-14

Query Match 97.4%; Score 1635; DB 6; Length 453;
Best Local Similarity 100.0%; Pred. No. 7.1e-140;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GLHQLSSPRYKFNFIADVVEKIPAVVHIELFLRHPFLFGHNPVPLSSGSGFIMSEAGLIIT 69
DB 129 GLHQLSSPRYKFNFIADVVEKIPAVVHIELFLRHPFLFGHNPVPLSSGSGFIMSEAGLIIT 188
QY 70 NAHVSSNSAAPGRQOLKVQLQNGDSYEATIKDIDKSDIATIKIHPKKLPVLLIGHSA 129
DB 189 NAHVSSNSAAPGRQOLKVQLQNGDSYEATIKDIDKSDIATIKIHPKKLPVLLIGHSA 248
QY 130 DLRPGEFVVAIGSPFALONTVTGIVSTAOREGRELGRSDMDYIQTDAIINYNGSGP 189
DB 249 DLRPGEFVVAIGSPFALONTVTGIVSTAOREGRELGRSDMDYIQTDAIINYNGSGP 308
QY 190 LVNLDGEVIGINTLKVTAIGISPAISDRITRFLTEFODKQIKDKKRFIGIRMTITPSL 249
DB 309 LVNLDGEVIGINTLKVTAIGISPAISDRITRFLTEFODKQIKDKKRFIGIRMTITPSL 368
QY 250 VDELKASNPDPPEVSSGIYQEVAPNSPSQSGIGIQDGIIVKNGRPLVDSSELQEAVALT 309
DB 369 VDELKASNPDPPEVSSGIYQEVAPNSPSQSGIGIQDGIIVKNGRPLVDSSELQEAVALT 428
QY 310 ESPLLLEVRKGNDDLFSIAPPEVVM 334
DB 429 ESPLLLEVRKGNDDLFSIAPPEVVM 453

RESULT 9
US-10-485-313A-27
Sequence 27, Application US/10485313A
GENERAL INFORMATION:
LOCUTION: (35)
APPLICANT: NIE, Guiying
APPLICANT: SALAMONSEN, Lois Adrienne
APPLICANT: LI, Ying
APPLICANT: HAMPTON, Anne Lorraine
APPLICANT: FINDLAY, John Kerr
TITLE OF INVENTION: Novel Serine Protease
FILE REFERENCE: 31633-200357

CURRENT APPLICATION NUMBER: US/10/485,313A
CURRENT FILING DATE: 2004-01-30
PRIOR APPLICATION NUMBER: PCT/AU02/01010
PRIOR FILING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: PR6707
PRIOR FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 459
TYPE: PRT
ORGANISM: Mus musculus
US-10-485-313A-27

Query Match 91.5%; Score 1536; DB 5; Length 459;
Best Local Similarity 92.6%; Pred. No. 7.4e-131;
Matches 302; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

QY 9 AGLHQLSSPRYKFNFIADVVEKIPAVVHIELFLRHPFLFGHNPVPLSSGSGFIMSEAGLIIT 68
DB 134 AGLHQLSSPRYKFNFIADVVEKIPAVVHIELFLRHPFLFGHNPVPLSSGSGFIMSEAGLIIT 193
QY 69 TNAHVSSNSAAPGRQOLKVQLQNGDSYEATIKDIDKSDIATIKIHPKKLPVLLIGHSA 128
DB 194 TNAHVSSNSAAPGRQOLKVQLQNGDSYEATIKDIDKSDIATIKIHPKKLPVLLIGHSA 253
QY 129 ADLRPEFVVAIGSPFALONTVTGIVSTAOREGRELGRSDMDYIQTDAIINYNGSGP 188
DB 254 ADLRPEFVVAIGSPFALONTVTGIVSTAOREGRELGRSDMDYIQTDAIINYNGSGP 313
QY 189 LVNLDGEVIGINTLKVTAIGISPAISDRITRFLTEFODKQIKDKKRFIGIRMTITPSL 248
DB 314 LVNLDGEVIGINTLKVTAIGISPAISDRITRFLTEFODKQIKDKKRFIGIRMTITPSL 373
QY 249 LVDELKASNPDPPEVSSGIYQEVAPNSPSQSGIGIQDGIIVKNGRPLVDSSELQEAVALT 308
DB 374 LVDELKASNPDPPEVSSGIYQEVAPNSPSQSGIGIQDGIIVKNGRPLVDSSELQEAVALT 433
QY 309 TESPLLEVRKGNDDLFSIAPPEVVM 334
DB 434 TESPLLEVRKGNDDLFSIAPPEVVM 459

RESULT 10
US-09-764-898-256
Sequence 256, Application US/09764898
Patent No. US20020090673A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P0201
CURRENT APPLICATION NUMBER: US/09/764,898
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 311
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 256
LENGTH: 286
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCUTION: (32)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCUTION: (35)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCUTION: (42)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCUTION: (104)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-764-898-256

Query Match 82.1%; Score 1378; DB 3; Length 286;
Best Local Similarity 98.6%; Pred. No. 9e-117;
Matches 275; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 56 GSGFMSEAGLITITNAHVSSNSAAPGKQOLKVQONQDSYEATIKDIDKSDIATIKIH 115
DB 8 GSGFMSEAGLITITNAHVSSNSAAPGKQOLKVQONQDSYEATIKDIDKSDIATIKIH 67
QY 116 PKKKLPVLLGHSADLRPEEFVAIGSPFALONTTGTIVSTAGREGELGRDSMDYI 175
DB 68 PKKKLPVLLGHSADLRPEEFVAIGSPFALONTTGTIVSTAGREGELGRDSMDYI 127
QY 176 QTDALINYGSGGPLVNLGDEVIGINTLKVTAISPAISDRITRFLTEFODKQIKDKK 235
DB 128 QTDALINYGSGGPLVNLGDEVIGINTLKVTAISPAISDRITRFLTEFODKQIKDKK 187
QY 236 RFLGIMRRTTTPSLVDELKASNDPFEVSGIYVQEVANSPSQRGIGDGDIIYKVNGR 295
DB 188 RFLGIMRRTTTPSLVDELKASNDPFEVSGIYVQEVANSPSQRGIGDGDIIYKVNGR 247
QY 296 PLVDSSELQEAVALTESPILLEVRGNDLLFSIAPEVVM 334
DB 248 PLVDSSELQEAVALTESPILLEVRGNDLLFSIAPEVVM 286

RESULT 11

US-10-301-822-79

; Sequence 79, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-10-301-822-79

Query Match 80.6%; Score 1353.5; DB 4; Length 452;
Best Local Similarity 86.1%; Pred. No. 3e-114;
Matches 285; Conservative 4; Mismatches 29; Indels 13; Gaps 3;

QY 10 GLHQLSSPRYKFNFIADVVEKIAPAVVHIELFLRHPFLGRNVPLSSGSGFMSEAGLIT 69
DB 129 GLHQLSSPRYKFNFIADVVEKIAPAVVHIELFLRHPFLGRNVPLSSGSGFMSEAGLIT 188
QY 70 NAHVSSNSAAPGKQOLKVQONQDSYEATIKDIDKSDIATIKIHPPKKLPVLLGHS 129
DB 189 NAHVSSNSAAPGKQOLKVQONQDSYEATIKDIDKSDIATIKIHPPKKLPVLLGHS 248
QY 130 DLPRGEFVAIGSPFALONTTGTIVSTAGREGELGRDSMDYIQTDAIINYG 183

DB 249 DLPRGSLWMPSESLRPTSHS-DNGIVALPSGQAGPPGLRHGHTSRM-----PSSNY 301

QY 184 GNSGGPLVNLGDEVIGINTLKVTAISPAISDRITRFLTEFODKQIKDKKRRIFGRM 243

DB 302 GNSGGPLVNLGDEVIGINTLKVTAISPAISDRITRFLTEFODKQIKDKKRRIFGRM 361

QY 244 TTPSLVDELKASNDPFEVSGIYVQEVANSPSQRGIGDGDIIYKVNGRPLVDSSEL 303

DB 362 TTPSLVDELKASNDPFEVSGIYVQEVANSPSQRGIGDGDIIYKVNGRPLVDSSEL 421

QY 304 QEAVALTESPILLEVRGNDLLFSIAPEVVM 334

DB 422 QEAVALTESPILLEVRGNDLLFSIAPEVVM 452

RESULT 12

US-10-485-313A-34

; Sequence 34, Application US/10485313A
; Publication No. US20050059002A1
; GENERAL INFORMATION:
; APPLICANT: NIE, Guiying
; APPLICANT: SALAMONSEN, Lois Adrienne
; APPLICANT: LI, Ying
; APPLICANT: HAMPTON, Anne Lorraine
; APPLICANT: FINDLAY, John Kerr
; TITLE OF INVENTION: Novel Serine Protease
; FILE REFERENCE: 31633-200357
; CURRENT APPLICATION NUMBER: US/10/485,313A
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: PCT/NO02/01010
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: PR6707
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-485-313A-34

Query Match 66.5%; Score 1117; DB 5; Length 357;
Best Local Similarity 100.0%; Pred. No. 7.1e-93;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GLHQLSSPRYKFNFIADVVEKIAPAVVHIELFLRHPFLGRNVPLSSGSGFMSEAGLIT 69

DB 129 GLHQLSSPRYKFNFIADVVEKIAPAVVHIELFLRHPFLGRNVPLSSGSGFMSEAGLIT 188

QY 70 NAHVSSNSAAPGKQOLKVQONQDSYEATIKDIDKSDIATIKIHPPKKLPVLLGHS 129

DB 189 NAHVSSNSAAPGKQOLKVQONQDSYEATIKDIDKSDIATIKIHPPKKLPVLLGHS 248

QY 130 DLPRGEFVAIGSPFALONTTGTIVSTAGREGELGRDSMDYIQTDAIINYGSG 189

DB 249 DLPRGEFVAIGSPFALONTTGTIVSTAGREGELGRDSMDYIQTDAIINYGSG 308

QY 190 LVNLGDEVIGINTLKVTAISPAISDRITRFLTEFODKQIK 221

DB 309 LVNLGDEVIGINTLKVTAISPAISDRITRFLTEFODKQIK 350

RESULT 13

US-09-764-898-184

; Sequence 184, Application US/09764898
; Patent No. US20020090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P201
; CURRENT APPLICATION NUMBER: US/09/764,898
; CURRENT FILING DATE: 2001-01-17


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; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 184
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (244)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (265)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-898-184

Query Match          65.8%; Score 1105; DB 3; Length 330;
Best Local Similarity 99.1%; Pred. No. 7.9e-92;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 GLHQLSSPRYKFNFIADVVEKIAPAVVAHIELFLRHPLGRNVPLSSGSGFTMSEAGLIIT 69
Db 102 GLHQLSSPRYKFNFIADVVEKIAPAVVAHIELFLRHPLGRNVPLSSGSGFTMSEAGLIIT 161
Qy 70 NAHVVSNSAAPGRQQLKVQLONGDSYEATIKDIDKSDIATIKIHPKKKLPVLLGHSA 129
Db 162 NAHVVSNSAAPGRQQLKVQLONGDSYEATIKDIDKSDIATIKIHPKKKLPVLLGHSA 221
Qy 130 DLRRGEFVVAIGSPFALQNTVTGIVSTAOREGRELGRSDMDYIQTDAIINYNSGSP 189
Db 222 DLRRGEFVVAIGSPFALQNTVTGIVSTAOREGRELGRSDMDYIQTDAIINYNSGSP 281
Qy 190 LVNLDEVIQINTLKVTAIGISFALPSDRITRFLTEFODKOIK 231
Db 282 LVNLDEVIQINTLKVTAIGISFALPSDRITRFLTEFODKOIK 323

RESULT 14
US-10-485-313A-39
; Sequence 39, Application US/10485313A
; Publication No. US20050059002A1
; GENERAL INFORMATION:
; APPLICANT: NIE, Guiling
; APPLICANT: SALAMONSEN, Lois Adrienne
; APPLICANT: LI, Ying
; APPLICANT: HAMPTON, Anne Lorraine
; APPLICANT: FINDLAY, John Kerr
; TITLE OF INVENTION: Novel Serine Protease
; FILE REFERENCE: 31633-200357
; CURRENT APPLICATION NUMBER: US/10/485,313A
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: PCT/AU02/01010
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: PR6707
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 39
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-485-313A-39

Query Match          63.0%; Score 1057; DB 5; Length 363;
Best Local Similarity 92.8%; Pred. No. 2.1e-87;
Matches 207; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

Qy 9 AGHQLSSPRYKFNFIADVVEKIAPAVVAHIELFLRHPLGRNVPLSSGSGFTMSEAGLIIT 68
Db 134 SGLHQLTSPRYKFNFIADVVEKIAPAVVAHIELFLRHPLGRNVPLSSGSGFTMSEAGLIIV 193
Qy 69 TNAHVVSNSAAPGRQQLKVQLONGDSYEATIKDIDKSDIATIKIHPKKKLPVLLGHSA 128
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Db 194 TNAHVVSNSSTAQRQQLKVQLONGDAYEATIKDIDKSDIATIVIHPPKKLPVLLGHSA 253
Qy 129 ADLRGEFVVAIGSPFALQNTVTGIVSTAOREGRELGRSDMDYIQTDAIINYNSGSP 188
Db 254 ADLRGEFVVAIGSPFALQNTVTGIVSTAORDKEGELGRSDMDYIQTDAIINYNSGSP 313
Qy 189 LVNLDEVIQINTLKVTAIGISFALPSDRITRFLTEFODKOIK 231
Db 314 LVNLDEVIQINTLKVTAAGISFALPSDRITRFLTEFODKIVK 356

RESULT 15
US-10-104-047-2765
; Sequence 2765, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2765
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2765

Query Match          61.6%; Score 1034.5; DB 4; Length 447;
Best Local Similarity 62.1%; Pred. No. 3.2e-85;
Matches 203; Conservative 60; Mismatches 55; Indels 9; Gaps 2;

Qy 10 GLHQLSSPRYKFNFIADVVEKIAPAVVAHIELFLRHPLGRNVPLSSGSGFTMSEAGLIIT 69
Db 125 GQEDPNSLRHKCNFIADVVEKIAPAVVAHIELFLRLPSKREVPVASSGSGFTVSEDEGLVIT 184
Qy 70 NAHVVSNSAAPGRQQLKVQLONGDSYEATIKDIDKSDIATIKIHPKKKLPVLLGHSA 129
Db 185 NAHVVTN-----KRVVVELKNGATYEAKIKDVERKADIALIKIDHGKLPVLLGRSS 238
Qy 130 DLRRGEFVVAIGSPFALQNTVTGIVSTAOREGRELGRSDMDYIQTDAIINYNSGSP 189
Db 239 ELRRGEFVVAIGSPFALQNTVTGIVSTQGRKELGRSDMDYIQTDAIINYNSGSP 298
Qy 190 LVNLDEVIQINTLKVTAIGISFALPSDRITRFLTEFODKOIKD--WKREFGIRMRITIT 246
Db 299 LVNLDEVIQINTLKVTAIGISFALPSDKIKFLTESHRQAKKAITKKKXITGIRMSLT 358
Qy 247 PSLVDELKASNPDPPEVSSGIYQEVAPNSPDRGIGQDGIIVKNGRPLVDSSELQEA 306
Db 359 SSKAKELKDRDRPDPVIGAYITEVIPDTBAEAGLKENDVIIISINQSVASANDVSDV 418
Qy 307 VLTESPLLETRRGNDLLFSIABEVV 333
Db 419 IKRSTLMVVRKGNEDIMITVPEEI 445
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Search completed: February 21, 2006, 21:16:20
Job time : 164 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 21, 2006, 21:13:46 ; Search time 18 Seconds

(without alignments)
264.225 Million cell updates/sec

Title: US-10-617-443B-2

Perfect score: 1679
Sequence: 1 MHLLPASPAGLHQLSSPRK.....LEVRGNDLLFSTAPEVVM 334

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 108093 seqs, 14239677 residues

Total number of hits satisfying chosen parameters: 108093

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
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5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1353.5	80.6	452	7	US-11-186-284-79 Sequence 79, Appl
2	1034.5	61.6	447	7	US-11-072-512-2765 Sequence 2765, Ap
3	1034.5	61.6	480	6	US-10-821-234-1465 Sequence 1465, Ap
4	882	52.5	458	7	US-11-183-914-11 Sequence 11, Appl
5	535	31.9	109	7	US-11-053-076-59 Sequence 59, Appl
6	496	29.5	100	7	US-11-107-096-78 Sequence 78, Appl
7	414	24.7	499	6	US-10-467-657-2096 Sequence 2096, Ap
8	410	24.4	474	7	US-11-098-686-10591 Sequence 10591, A
9	360.5	21.5	441	6	US-10-454-437-56 Sequence 56, Appl
10	335.5	20.0	423	7	US-11-074-176-4 Sequence 4, Appl
11	318	18.9	317	6	US-10-793-626-1824 Sequence 1824, Ap
12	260.5	15.5	493	6	US-10-793-626-1832 Sequence 1832, Ap
13	259.5	15.5	115	6	US-10-485-788A-774 Sequence 774, App
14	259.5	15.5	115	7	US-11-053-076-152 Sequence 152, App
15	239	12.2	101	7	US-11-107-096-77 Sequence 77, Appl
16	214.5	12.8	99	7	US-11-107-096-79 Sequence 79, Appl
17	204	12.2	100	7	US-11-107-096-1 Sequence 1, Appl
18	200.5	11.9	97	7	US-11-053-076-60 Sequence 60, Appl
19	189	11.3	109	6	US-10-485-788A-805 Sequence 805, App
20	189	11.3	109	7	US-11-053-076-188 Sequence 188, App
21	128	7.6	397	6	US-10-454-437-60 Sequence 60, Appl
22	122	7.3	238	6	US-10-485-517-191 Sequence 191, Appl
23	120	7.1	217	7	US-11-019-711-136 Sequence 136, App
24	116.5	6.9	239	6	US-10-485-517-192 Sequence 192, App
25	116.5	6.9	239	6	US-10-485-517-195 Sequence 195, App

26	116.5	6.9	239	6	US-10-485-517-323 Sequence 323, App
27	115.5	6.9	241	6	US-10-485-517-189 Sequence 189, App
28	114	6.8	180	6	US-10-485-517-194 Sequence 194, App
29	114	6.8	180	6	US-10-485-517-322 Sequence 322, App
30	113.5	6.8	247	6	US-10-485-517-190 Sequence 190, App
31	111.5	6.6	227	7	US-11-151-601-36 Sequence 36, Appl
32	111.5	6.6	249	7	US-11-151-601-28 Sequence 28, Appl
33	111.5	6.6	251	7	US-11-151-601-27 Sequence 27, Appl
34	107	6.4	254	6	US-10-485-517-188 Sequence 188, App
35	107	6.4	1183	7	US-11-115-639-18 Sequence 18, Appl
36	106	6.3	1183	7	US-11-115-639-15 Sequence 15, Appl
37	106	6.3	1183	7	US-11-115-639-17 Sequence 17, Appl
38	105	6.3	2759	6	US-10-453-372-168 Sequence 168, App
39	104	6.2	1183	7	US-11-115-639-13 Sequence 13, Appl
40	103	6.1	1183	6	US-10-793-626-568 Sequence 568, App
41	100	6.0	1183	7	US-11-115-639-16 Sequence 16, Appl
42	100	6.0	4384	6	US-10-821-234-1120 Sequence 1120, Ap
43	99.5	5.9	282	6	US-10-793-626-364 Sequence 364, App
44	98.5	5.9	1183	7	US-11-115-639-14 Sequence 14, Appl
45	97.5	5.8	442	7	US-11-098-686-11368 Sequence 11368, A

ALIGNMENTS

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RESULT 1
US-11-186-284-79
; Sequence 79, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MEMO1-029P2RNM
; CURRENT FILING DATE: 2005-07-21
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/11/186,284
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-79

Query Match      80.6%   Score 1353.5; DB 7; Length 452;
Best Local Similarity 86.1%; Pred. No. 8.8e-108;
Matches 285; Conservative 4; Mismatches 23; Indels 13; Gaps 3;

QY      10  GHHQLSSPRYKFNFIADYVEKIPAVVAHIEFLRHPFLGRNVPLSSGSGFTMSEAGLIIT 69
      |||
DB      129  GHHQLSSPRYKFNFIADYVEKIPAVVAHIEFLRHPFLGRNVPLSSGSGFTMSEAGLIIT 188
      |||

QY      70  NHHVYSSNSAPAGROQLKVOQLNGDSYRATIKDKIDSKDITIKHPKKKLPVLLGGHSA 129
      |||
DB      189  NHHVYSSNSAPAGROQLKVOQLNGDSYRATIKDKIDSKDITIKHPKKKLPVLLGGHSA 248
      |||

QY      130  DLRPFEFVVAIGSPFALQNTVTTGIVST-----AQREGREIGLRDSMDYIQTDALINY 183
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Db 249 DLAVGSLMPSESLRPTREHS-DNGIYVALPSGGQAGPGLRHGHTRRM-----PSNV 301
Qy 184 GNSGGPLVNLDEGVIGINTLKTAGISFALPSDRITRFLTEFODKQIKCKKRFIGIR 243
Db 302 GNSGGPLVNLDEGVIGINTLKTAGISFALPSDRITRFLTEFODKQIKCKKRFIGIR 361
Qy 244 TTPSLVDELKASNPDPPEVSSGIYVOEVAPNSPSQSGIOPDGIYKVGRLVDSSEL 303
Db 362 TTPSLVDELKASNPDPPEVSSGIYVOEVAPNSPSQSGIOPDGIYKVGRLVDSSEL 421
Qy 304 QEAULTESPLLEVRGNDLLEFSIAPEVVM 334
Db 422 QEAULTESPLLEVRGNDLLEFSIAPEVVM 452

RESULT 2
US-11-072-512-2765
; Sequence 2765, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YUKI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOTIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072, 512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350, 978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379296
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2765
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2765

Query Match 61.6%; Score 1034.5; DB 7; Length 447;
Best Local Similarity 62.1%; Pred. No. 1.3e-80;
Matches 203; Conservative 60; Mismatches 55; Indels 9; Gaps 2;

Qy 10 GLHQLSPRYKPNFADVVEKIAPAVNHIELFLRHLFGRAWPLSSGSGFIMSEAGLIT 69
Db 125 GQEDPNSLRHKXNFADVVEKIAPAVNHIELFLRHLFGRAWPLSSGSGFIMSEAGLIT 184
Qy 70 NAHVSSNSAAPGRQOLKVOLONGDSEYATIKDIDKSDIATIKIHPPKKKLPVLLIGHSA 129
Db 185 NAHVNTN-----KRVKVELKNGATYEAKIKVDDEKADIALIKIDHGKLEVLILGRSS 238
Qy 130 DLRPGEFVVAIGSPFALONTVTTGTIVSTAQREGRELGRLSDMDYIQTDAIINYGNSGSP 189
Db 239 ELRPGEFVVAIGSPFALONTVTTGTIVSTAQREGRELGRLSDMDYIQTDAIINYGNSGSP 298
Qy 190 LVNLGDEVIGINTLKTAGISFALPSDRITRFLTEFODKQIKCKKRFIGIRMTIT 246
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Db 299 LVNLGDEVIGINTLKTAGISFALPSDRITRFLTEFODKQIKCKKRFIGIRMTIT 358
Qy 247 PSVLDELKASNPDPPEVSSGIYVOEVAPNSPSQSGIOPDGIYKVGRLVDSSELQEA 306
Db 359 SSKAKELKDRHRDPFDVIGAYIIEVTPDAEAGLGKENDVITISINGQSVASANDVSDV 418
Qy 307 VLTESPLLEVRGNDLLEFSIAPEVVM 333
Db 419 IKRSTLMVVRGNDIMITVPEEI 445

RESULT 3
US-10-821-234-1465
; Sequence 1465, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labac, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PL SEQ_genes Version 1.0
; SEQ ID NO 1465
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1465

Query Match 61.6%; Score 1034.5; DB 6; Length 480;
Best Local Similarity 62.1%; Pred. No. 1.4e-80;
Matches 203; Conservative 60; Mismatches 55; Indels 9; Gaps 2;

Qy 10 GLHQLSPRYKPNFADVVEKIAPAVNHIELFLRHLFGRAWPLSSGSGFIMSEAGLIT 69
Db 158 GQEDPNSLRHKXNFADVVEKIAPAVNHIELFLRHLFGRAWPLSSGSGFIMSEAGLIT 217
Qy 70 NAHVSSNSAAPGRQOLKVOLONGDSEYATIKDIDKSDIATIKIHPPKKKLPVLLIGHSA 129
Db 218 NAHVNTN-----KRVKVELKNGATYEAKIKVDDEKADIALIKIDHGKLEVLILGRSS 271
Qy 130 DLRPGEFVVAIGSPFALONTVTTGTIVSTAQREGRELGRLSDMDYIQTDAIINYGNSGSP 189
Db 272 ELRPGEFVVAIGSPFALONTVTTGTIVSTAQREGRELGRLSDMDYIQTDAIINYGNSGSP 331
Qy 190 LVNLGDEVIGINTLKTAGISFALPSDRITRFLTEFODKQIKCKKRFIGIRMTIT 246
Db 332 LVNLGDEVIGINTLKTAGISFALPSDRITRFLTEFODKQIKCKKRFIGIRMTIT 391
Qy 247 PSVLDELKASNPDPPEVSSGIYVOEVAPNSPSQSGIOPDGIYKVGRLVDSSELQEA 306
Db 392 SSKAKELKDRHRDPFDVIGAYIIEVTPDAEAGLGKENDVITISINGQSVASANDVSDV 451
Qy 307 VLTESPLLEVRGNDLLEFSIAPEVVM 333
Db 452 IKRSTLMVVRGNDIMITVPEEI 478

RESULT 4
US-11-183-914-11
; Sequence 11, Application US/11183914
; Publication No. US20050282214A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
```

APPLICANT: Tang, Tom Y.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/183,914
FILING DATE: 19-JULY-2005
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SINITCT01
CLONE: 2680548
US-11-183-914-11

Query Match 52.5%; Score 882; DB 7; Length 458;
Best Local Similarity 52.5%; Pred. No. 1.3e-67;
Matches 169; Conservative 72; Mismatches 71; Indels 10; Gaps 2;

QY 15 SSPPKFNFIADVVEKIPAVVHLEFLRHPFLGRNVPFLSSGSGFIMSEAGLIITNAHV 74
DB 141 ASPPSQNFIVADVVEKIPAVVHLEFLRHPFLGRNVPFLSSGSGFIMSEAGLIITNAHV 200
QY 75 SSNSAAPGRQOLKVLQNGDSYEATIKDIDKSDIATIKIHPKKKLPVLLIGHSADLRPG 134
DB 201 AD-----RRRVRVRLISGDTYEAVVTAADPVADIAATRIQTKEPLPTLPLGRSADVROG 254
QY 135 EFVVAIGSPFLQNTTGTIVSTAGREBELGLRSDMDYIQTDAIINYKNSGGLVNLMD 194
DB 255 EFVVAIGSPFLQNTTGTIVSTAGREBELGLRSDMDYIQTDAIINYKNSGGLVNLMD 314
QY 195 GEVGINFLKTAGISFAIPSDRITRFLTEFODKQ-----IDWKKRFIGIRNRITTPSLV 250
DB 315 GEVGINFLKTAGISFAIPSDRITRFLTEFODKQ-----IDWKKRFIGIRNRITTPSLV 374
QY 251 DELKASNDPPEVSSGIVYQEAAPSPOGIGIDGDIIVKNGRPLVDSSELQAVLITE 310
DB 375 AELDREPSFPDVQGHVLIHVYILGSPFAHRAGLRPGDVILAIIGEQVONADVEVAVATQ 434
QY 311 SPILLEVRGNDLLFSIAPEV 332
DB 435 SOLAVQIRKREKTLIVTPEV 456

RESULT 5

US-11-053-076-59
Sequence 59, Application US/11053076
Publication No. US20050255460A1
GENERAL INFORMATION:
APPLICANT: Lu, Peter S.
APPLICANT: Schweizer, Johannes
APPLICANT: Somoza Diaz-Sarmiento, Chamorro
APPLICANT: Belmares, Michael P.
TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
FILE REFERENCE: VITA-008CIP
CURRENT APPLICATION NUMBER: US/11/053,076
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: PCT/US03/28508
PRIOR FILING DATE: 2003-09-09
PRIOR APPLICATION NUMBER: 10/630,590
PRIOR FILING DATE: 2003-07-29
PRIOR APPLICATION NUMBER: 60/490,094
PRIOR FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: 60/450,464
PRIOR FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: 60/409,298
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 10/630,590
PRIOR FILING DATE: 2003-07-29
PRIOR APPLICATION NUMBER: PCT/US02/24655
PRIOR FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: 60/309,841
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 60/360,061
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 10/080,273
PRIOR FILING DATE: 2002-02-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 59
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-11-053-076-59

Query Match 31.9%; Score 535; DB 7; Length 109;
Best Local Similarity 100.0%; Pred. No. 5.7e-39;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 LTFEODKQIKQWKRRFIRNRITTPSLVDELKASNDPPEVSSGIVYQEAAPSPOG 281
DB 1 LTFEODKQIKQWKRRFIRNRITTPSLVDELKASNDPPEVSSGIVYQEAAPSPOG 60
QY 282 GIDGDIIVKNGRPLVDSSELQAVLITESPLLEVRGNDLLFS 327
DB 61 GIDGDIIVKNGRPLVDSSELQAVLITESPLLEVRGNDLLFS 106

RESULT 6

US-11-107-096-78
Sequence 78, Application US/11107096
Publication No. US20060003348A1
GENERAL INFORMATION:
APPLICANT: ZHANG, YINGNAN
APPLICANT: SIDHU, SACHDEV S.
TITLE OF INVENTION: CMT PDZ MODULATORS
FILE REFERENCE: P2100R1
CURRENT APPLICATION NUMBER: US/11/107,096
CURRENT FILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: US 60/563,157
PRIOR FILING DATE: 2004-04-16
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 78
LENGTH: 100
TYPE: PRT
ORGANISM: Homo sapiens
US-11-107-096-78

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/ TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
/ TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
/ FILE REFERENCE: 09531-128001
/ CURRENT APPLICATION NUMBER: US/11/098,686
/ CURRENT FILING DATE: 2005-04-04
/ PRIOR APPLICATION NUMBER: PCT/US03/31318
/ PRIOR FILING DATE: 2003-10-01
/ PRIOR APPLICATION NUMBER: US 60/416,395
/ PRIOR FILING DATE: 2002-10-04
/ NUMBER OF SEQ ID NOS: 11433
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10591
/ LENGTH: 474
/ TYPE: PRT
/ ORGANISM: Lawsonia intracellularis
/
Query Match          24.4%; Score 410; DB 7; Length 474;
Best Local Similarity 35.5%; Pred. No. 2,1e-27;
Matches 94; Conservative 58; Mismatches 89; Indels 24; Gaps 7;
/
Db      54  SSGSGFMSEAGLIITNAHVSSNSAAPGRQQLKVQLQ---NGDSYEATIKQIDKSDI 109
      91  SLGGLFISSDGYIVTNHNYLE-----GADSVRVNLEGRSGKESLPAEVIGRDEFTLD 144
/
Db      110  ATTIHPKKLPVLLHGSADLRGEVVAIGSPFALQNTVYTGIVSTAOREGELGRD 169
      145  ALLKVKSKDSLPIYIFGNSDIMEGEVWLAIGNFPGHVTYAGILBA---KGRDHAP 201
/
Db      170  SDMWYIGTDAIINVGNSGGPVLVNDGEVIGINTLKVTA--GISPAISDRITRFLTEFOD 227
      202  FD-NFLQTDASINGNSSGGPFLINSGGVGINTALMASGGIGALITSSMAADRIEQL-- 258
/
Db      228  KQIKDWKKRFPIGRMRTITPSLVDELKASNPDPFEVSSGIYVOEVAAPSQRCIGDGD 287
      259  KTNKVKSRGWIQVITQVDVNTAKALGSLQ-----AKGALVGSVVEGDPADKAKLKVGD 312
/
Db      288  IIVKVNRPVLVDSELOEAVITESP 312
      313  IVTQADGKQIDASASLLKAIATKPP 337
/
RESULT 9
US-10-454-437-56
/ Sequence 56, Application US/10454437
/ Publication No. US20050277115A1
/ GENERAL INFORMATION:
/ APPLICANT: Pompeius, Markus
/ APPLICANT: Kroger, Burkhard
/ APPLICANT: Schröder, Hartwig
/ APPLICANT: Zelder, Oskar
/ APPLICANT: Haberhauser, Gregor
/ TITLE OF INVENTION: CORNEIBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
/ TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPATION
/ FILE REFERENCE: BGI-128CPCN
/ CURRENT APPLICATION NUMBER: US/10/454,437
/ CURRENT FILING DATE: 2003-06-13
/ PRIOR APPLICATION NUMBER: US 60/141031
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: DE 19931536.8
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19932125.6
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932126.4
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932127.2
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932128.0
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932129.9
/ PRIOR FILING DATE: 1999-07-19
/ PRIOR APPLICATION NUMBER: DE 19932226.0
/ PRIOR FILING DATE: 1999-07-09
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; PRIOR APPLICATION NUMBER: DE 19932920.6
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: DE 19932922.2
 ; PRIOR FILING DATE: 1999-07-14
 ; Remaining Prior Application data removed - See file Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 442
 ; SEQ ID NO 56
 ; LENGTH: 441
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 ; US-10-454-437-56

Query Match 21.5%; Score 360.5; DB 6; Length 441;
 Best Local Similarity 34.5%; Pred. No. 3.2e-23;
 Matches 101; Conservative 44; Mismatches 97; Indels 51; Gaps 9;

QY 27 VKEIAPVAVHIEFLRHPFLFGRNVLSSGSGFIMSEAGLITNAHVSSNSAPGRQO- 85
 DB 146 VAAAVLPVSVISQAIATR-----TSASBGSGSISSDGYVTNNHVA-----GIBQS 192
 QY 86 --LKVQLONGDSYEATIDIDKSDIATIKHPKKLPVLLGHADLRPFVVAIGSP 143
 DB 193 GVLEVSFSDGTTAQDFIAGDSTDAVIRKRVSNLPMVSFGSDDALGVQSVAAVAGSP 252
 QY 144 FALQNTTGTGIVSTQREGREL--GLRDSMDYIQTDAIINNGSGPLVNLDEGVIGIN 201
 DB 253 LGLSTVTGTGIVSAVNRPRASGDGESSLIDAIQTDAIINNGSGPLVMDGNLIGMN 312
 QY 202 TLKV-----TAGISFALPSDRITRFLTEFODKOIKWK--KRFIGIMRTITPSL 249
 DB 313 SVIASISSTSDSAGSIGLGFISPSN----FAKRVADQLISTQVQPMIGVQGT----- 363
 QY 250 VDELKASNPDPPEVSSGIYQVEAVNPSQKGIQDSDIIVKNGRPLVDSSE 302
 DB 364 -----DNSVTGAVIASVODGPGADAGLQPGDGIYVTKLNDLR-VIDSPD 404

RESULT 10
 US-11-074-176-4
 ; Sequence 4, Application US/11074176
 ; Publication No. US20050250135A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Klaenhammer, Todd R.
 ; APPLICANT: Russell, William M.
 ; APPLICANT: Alterman, Eric
 ; APPLICANT: McAuliffe, Olivia
 ; APPLICANT: Perill, Andrea Azcarate
 ; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
 ; FILE REFERENCE: 5051-694
 ; CURRENT APPLICATION NUMBER: US/11/074,176
 ; CURRENT FILING DATE: 2005-03-07
 ; PRIOR APPLICATION NUMBER: 60/551,161
 ; PRIOR FILING DATE: 2004-03-08
 ; NUMBER OF SEQ ID NOS: 381
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 423
 ; TYPE: PRT
 ; ORGANISM: Lactobacillus acidophilus
 ; US-11-074-176-4

Query Match 20.0%; Score 335.5; DB 7; Length 423;
 Best Local Similarity 30.6%; Pred. No. 4e-21;
 Matches 95; Conservative 54; Mismatches 114; Indels 47; Gaps 11;

QY 48 GRNVLSGSGGFIMSEA---GLITNAHVSSNSAPGRQOLQNGDSYEATIKDID 104
 DB 133 GLEETYSSESSVYVWKSNGKGIYVTNNHVISGSDA-----VQVQLANGKTVSAKAVGKD 186
 QY 105 KKSADIATIKHPKKLPVLLGHADLRPFGEFVVAIGSPFALO--NTVTTGIVSTQAR-- 160
 DB 187 STTDLAVSIDAKVYTGTAEFSDSKSLQAGGVIAVSGPLSGEYASTVYGGIISAPARTI 246

QY 161 ---EGRELGLRDSMDYIQTDAIINNGSGPLVNLDEGVIGINTLKY-----TAGI 209
 DB 247 STSSGNO-----QTVIQTDAIINPGNSGALVNSAQVIGINSMKLAQSSDGTSVGKM 299
 QY 210 SPFAPSDRITRFLTEFODKOIKWK--KRFIGIR---MRTITPSLVDELKASNPDPPEVS 264
 DB 300 GPALPSNEVTVITNEL-----VKKGKITRPGQGVRAVLEGIPEAVRSRLKIKS-----NLK 351
 QY 265 SGIVQVEAVNPSQKGIQDSDIIVKNGRPLVDSSELQNAVLT---SPILLEVRGN 321
 DB 352 SGIVYASINKNSAANAMKSGDVITKVDGKVDVASHLSILYSHKVGDTVNTINRNG 411
 QY 322 DDLLEFSIAPE 331
 DB 412 RDVNLKVLGE 421

RESULT 11
 US-10-793-626-1824
 ; Sequence 1824, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PUS480US
 ; CURRENT APPLICATION NUMBER: US/10/793,626
 ; CURRENT FILING DATE: 2004-03-04
 ; PRIOR APPLICATION NUMBER: 60/164,258
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1824
 ; LENGTH: 317
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; US-10-793-626-1824

Query Match 18.9%; Score 318; DB 6; Length 317;
 Best Local Similarity 31.9%; Pred. No. 8.1e-20;
 Matches 86; Conservative 57; Mismatches 79; Indels 48; Gaps 11;

QY 56 GSGFI--MSF-AGLITNAHVSSNSAPGRQOLQNGDSYEATIKDIDKSDIARTI 112
 DB 27 GSGVYQISEGSAYIVTNNHVD-----GASBIKVLQHSKQYDAKLIGDALTDIAVL 80
 QY 113 KHPKKLPVLLGHADLRPFGEFVVAIGSPFALO--NTVTTGIVSTQAR-GRGLARD 169
 DB 81 KIKDTKGKAIQFANSSVQGTDSVPFAGNPLGFAPASVTSGLISASERTIDANTSAGN 140
 QY 170 SMDYIQTDAIINNGSGPLVNLDEGVIGINTLKVTA---GISFALPSDRITRFLTEF 225
 DB 141 TKAVNLQTDALINNGSGALVDINGNLVGNISKIAAQAQVGEIGFALPSNEVARTI--- 197
 QY 226 QDKQIKWK--KRFIGIMRTITPSLVDELKASNPDPPE-----VSSGIYQVEAVP 274
 DB 198 -EQLVKHGKIRPSIGIGLIMNS-----DIPENRKEIHTKDKGVVAVAKV-- 242
 QY 275 NSPQKGIQDSDIIVKNGRPLVDSSELQ 304
 DB 243 ---DSENAIKKGKIDITIGDKQIKDDTDLR 269

RESULT 12
 US-10-793-626-1832
 ; Sequence 1832, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

; CURRENT APPLICATION NUMBER: US/11/107,096
 ; CURRENT FILING DATE: 2005-04-15
 ; PRIOR APPLICATION NUMBER: US 60/563,157
 ; PRIOR FILING DATE: 2004-04-16
 ; NUMBER OF SEQ ID NOS: 79
 ; SEQ ID NO 77
 ; LENGTH: 101
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-107-096-77

Query Match 14.2%; Score 239; DB 7; Length 101;
 Best Local Similarity 40.4%; Pred. No. 8.3e-14;
 Matches 40; Conservative 32; Mismatches 27; Indels 0; Gaps 0;

Qy 235 KRFIGIRNRITTPSLVDELKASNPDPPEVSSGIYQEVAPNSPSQSGIODGDIIVKXNG 294
 Db 1 KKYIGIRNMSLTSSKAKELKDRHRDPDVIGAYTIEVLPPTPAEAGGKENDVITISNG 60
 Qy 295 RPLVDSELQEAVALTESPILLLEVRGRNDLFSIAPEVY 333
 Db 61 QSVVSANDVSDVIKRESTLNWVRGRNEDIMITVIEBI 99

Search completed: February 21, 2006, 21:16:43
 Job time : 19 secs

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GenCore version 5.1.7
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OM protein - nucleic search, **using frame 2**

Run on: February 21, 2006, 20:12:52 ; Search time 208 Seconds

(without alignments)
2854.354 Million cell updates/sec

Title: US-10-617-443B-2

Perfect score: 1679

Sequence: 1 MHLLPASPAGHQLSSPRK.....LEVRGNDLLFSLAPEVVM 334

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Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abs03p -USER=US10617443 @CGN_1_1_290 @runat_21022006_165823_17255
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-DEV TIMEOUT=130 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:
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2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1034.5	61.6	1521	3	US-09-949-016-4643 Sequence 4643, App
2	1034.5	61.6	1894	3	US-10-104-047-795 Sequence 795, App
3	1034.5	61.6	2036	3	US-09-949-016-1399 Sequence 399, App
4	1034.5	61.6	2205	3	US-08-888-077A-41 Sequence 41, App
5	1027.5	61.2	2036	3	US-08-923-454A-17 Sequence 17, App
6	920	54.8	1859	3	US-09-724-864-22 Sequence 22, App
7	882	52.5	1835	3	US-08-923-454A-7 Sequence 7, App
8	882	52.5	2040	3	US-09-075-460-4 Sequence 4, App
9	882	52.5	2187	3	US-08-923-454A-23 Sequence 23, App

10	882	52.5	2187	3	US-08-923-454A-24	Sequence 24, App
11	882	52.5	2476	3	US-09-008-271A-23	Sequence 23, App
12	882	52.5	2476	3	US-09-968-415-23	Sequence 23, App
13	878	52.3	2187	3	US-08-923-454A-30	Sequence 30, App
14	834.5	49.7	1787	3	US-08-923-454A-3	Sequence 3, App
15	834.5	49.7	2551	3	US-08-923-454A-26	Sequence 26, App
16	779	46.4	1503	3	US-08-923-454A-5	Sequence 5, App
17	779	46.4	2144	3	US-08-923-454A-28	Sequence 28, App
18	579.5	34.5	539	2	US-08-322-742-18	Sequence 18, App
19	454	27.0	1230230	3	US-09-438-185A-1	Sequence 1, App
20	450.5	26.8	1425	3	US-09-489-039A-6523	Sequence 6523, App
21	444	26.4	1332	3	US-09-902-540-4672	Sequence 4672, App
22	444	24754	1332	3	US-09-902-540-1230	Sequence 1230, App
23	441.5	26.3	1368	3	US-09-711-164-245	Sequence 245, App
24	437	26.0	1386	3	US-09-902-540-4598	Sequence 4598, App
25	437	26.0	27707	3	US-09-902-540-1226	Sequence 1226, App
26	431	25.7	1068	3	US-09-711-164-246	Sequence 246, App
27	430	25.6	1230025	3	US-09-198-452A-1	Sequence 1, App
28	428	25.5	1436	3	US-09-199-637A-131	Sequence 131, App
29	425	25.3	1428	3	US-09-252-991A-12923	Sequence 12923, App
30	425	25.3	1455	3	US-09-252-991A-12561	Sequence 12561, App
31	424	25.3	732	3	US-08-923-454A-1	Sequence 1, App
32	422	25.1	1980	2	US-08-350-741-1	Sequence 1, App
33	422	25.1	1980	2	US-08-463-875A-1	Sequence 1, App
34	418	24.9	1500	3	US-09-673-898-5	Sequence 5, App
35	417	24.8	1083	3	US-09-489-039A-6463	Sequence 6463, App
36	415	24.7	1110	3	US-09-673-898-7	Sequence 7, App
37	414	24.7	1242	3	US-09-388-090-5	Sequence 5, App
38	414	24.7	1326	3	US-09-388-089B-13	Sequence 13, App
39	414	24.7	1395	3	US-09-388-089B-10	Sequence 10, App
40	414	24.7	1395	3	US-09-388-090-3	Sequence 3, App
41	414	24.7	1611	2	US-08-485-569-1	Sequence 1, App
42	414	24.7	1611	2	US-08-480-993-1	Sequence 1, App
43	414	24.7	1611	2	US-07-903-079B-1	Sequence 1, App
44	413	24.6	1830121	3	US-09-557-884-1	Sequence 1, App
45	413	24.6	1830121	3	US-09-643-990A-1	Sequence 1, App

ALIGNMENTS

RESULT 1
US-09-949-016-4643
Sequence 4643, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4643
LENGTH: 1521
TYPE: DNA
ORGANISM: Human
US-09-949-016-4643
Alignment Scores:
Pred. No.: 7.27e-111
Score: 1034.50
Percent Similarity: 80.44
Best Local Similarity: 62.14
Query Match: 61.64
DB: 3
Matches: 1521
Conservative: 203
Mismatches: 55
Indels: 9
Gaps: 2


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Db      999  AAGTCCATGACCGCAGCGCCAAAGGAAAGAACGCATCACAAGAAAGATATGTGTATC 1058
Qy      241  ArgwetaargthrllethThProSerleuValaBpGluLeuLysAlaSerAsnProAapPhe 260
Db      1059  CGAAATGAATGTCACACTACGTCGCCAGCAAGCCAAAGAGCTTAAGACCGGACCTTC 1118
Qy      261  ProGluValaSerSeGlyYrleThrValaGlnGluValaAlaProAsnSerProSerGlnArg 280
Db      1119  CGAGACGGATCTCAGAGACCGGTATATTAATTGAAGTATATTCCTGATATCCCGCAGAAAGCT 1178
Qy      281  GllgYlilleglnAspGlyAapIlelleValLysAlaSnGlyArgProleuValaBpSer 300
Db      1179  GGTGTCTCAAGAAAGAACGACGTCATTAATCAGATCATATGACACAGTCCGAGTCTCCGCC 1238
Qy      301  SerGluLeuGlnGluValaValleuthrGluSerProleuLeuLeuGluValaAlaArgArgly 320
Db      1239  AATGATGTCACGACGCTCATTTAAAGGAAAGACCCCTAACAATGTGTGTCCGACAGGGGT 1298
Qy      321  AsnAspAapleuLeuPheSerIleAlaProGluValaVal 333
Db      1299  AATGAAGATATCATGATCATCAGCTGATTTCCGAAAGAAATT 1337

RESULT 3
US-09-949-016-399
; Sequence 399, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMERPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FaastSeq for windows Version 4.0
; SEQ ID NO 399
; LENGTH: 2036
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-399

Alignment Scores:
Pred. No.:      1,14e-110      Length:      2036
Score:          1034.50      Matches:      206
Percent Similarity: 80.2%      Conservative: 61
Best Local Similarity: 61.9%      Mismatches:  57
Query Match:     61.6%      Indels:      10
DB:              3          Gaps:           2

US-10-617-443B-2 (1-334) x US-09-949-016-399 (1-2036)
Qy      4  AlaleuProAlaSerAlaGlyLeuHisGlnLeuSerSerProArgYrlyPheAsnPhe 23
Db      503  GCGGAGCCCTCGCGCCAAAGGCGAG-GAAGATCCCAAGATTTGGCCCTAATAATTAACTTT 561
Qy      24  lleaAlaBpValaValaGlnLysIleAlaProAlaValaValHisIleGlnLeuPheLeuArg 43
Db      562  ATGCGCGCAGGTGTGGAGAAAGATCGCCCTCGCGGTGTATATCGAATTTGTTCCGAAAG 621
Qy      44  HisProLeuPheGlyArgAsnValProLeuSerSerGlyYrlyPheIleMetSerGlu 63
Db      622  CTTCCGTTTCTTAAACGAAGAGTGCGCGGTGCTAGTGGGTCTGGGATTATATGTGCGAA 681
Qy      64  AlaGlyLeuIleIleThrAsnAlaHisValaValaSerSerAsnSerAlaAlaProGlyArg 83
Db      682  GATGACTATATGTGTGCAAAATGCCCACGTGTGTAACAA-----AAG 723

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01 84 GlnGlnLeuValAlaGlnLeuGlnAsnGlyAspSerTyrGluValAlaThrIleAspIle 103
02      :::::::::::::::::::::
03 724 CACC GGCGTCAAGATTGAGCTGAAGAAGCGTCCACTTACGAAGCCAAATCAAGATG 783
04
05 104 AspIlySerAspIleAlaThrIleIleIleHisProIySlyIyLeuProValLeu 123
06      :::::::::::::::::::::
07 784 GATGAGAAAGACAGACATCGACTCATCAAAATTGACCAAGGGCGACCTGCTCTCCG 843
08
09 124 LeuLeuGlyIleSerAlaAspLeuArgProGlyGluPheValValAlaIleGlySerPro 143
10      :::::::::::::::::::::
11 844 CTGCTGGCCCGCTCTCCAGAGCTGGCGGAGATTTCGTGTCGCATTCGAAGCCCG 903
12
13 144 PheAlaIleuGlnAsnThrValThrThyGlyIleValSerThrAlaGlnArgGluGlyArg 163
14      :::::::::::::::::::::
15 904 TTTTCCCTTCAAAACACAGTACCAACCGGGATTCGAGACACACACCACGAGCGGCAAA 963
16
17 164 GluLeuGlyLeuArgAspSerAspMetAspTyrIleGlnThrAspAlaIleIleAsnTyr 183
18      :::::::::::::::::::::
19 964 GAGCTGGGGGCTCCGCAACTCAGACATGAGACTATACCAACGACGACCATCATCACTAT 1022
20
21 184 GlyAsnSerGlyGlyProLeuValAsnLeuAspGlyGluValIleGlyIleAsnThrLeu 203
22      :::::::::::::::::::::
23 1024 GGAACCTCGGAGGGCCCGTTAGTAACTCGACCGGTGAAGATGGAATTAACTTTG 1082
24
25 204 LysValThrAlaGlyIleSerPheAlaIleProSerAspArgIleThrArgPheLeuThr 223
26      :::::::::::::::::::::
27 1084 AAGTGAAGAGCTGGGAATCTCTTGCAATCCCATCTGATGATTAAGATTAAAGTTCTCAGC 1142
28
29 224 GluPheGlnAspIySglnIleIyAsp-----TpyLSyArgPheIleGlyIle 240
30      :::::::::::::::::::::
31 1144 GAGTCCCATGACCCAGACAGCCCAAGAAAGCCATCACCAAGAAAGATATTTGGTATC 1202
32
33 241 ArgMetArgThrIleThrProSerLeuValAspGluLeuIySglnSerAsnProAspPhe 260
34      :::::::::::::::::::::
35 1204 CGAATGATGTCACTCACTCCAGCAAAAGCCAAAGCTGGAAGAGCCGACCGGGAGCTTC 1262
36
37 261 ProGluValSerSerGlyIleTyrValGlnGluValAlaProAsnSerProSerGlnArg 280
38      :::::::::::::::::::::
39 1264 CCAGACGGATCTCCAGAGCGGATATTAATTGAAGTAAATTCCTGATATACCCACAGAAAGCT 1322
40
41 281 GlyGlyIleGlnAspGlyAspIleIleValIySglnArgIyArgProLeuValAspSer 300
42      :::::::::::::::::::::
43 1324 GGTGATCTCAAGAAAGACAGCTCTAATACAGCATCATGACAGTCCGTGATCTCCGCC 1382
44
45 301 SerGluLeuGlnGluAlaValLeuThrGluSerProLeuLeuGluValIyArgArgGly 320
46      :::::::::::::::::::::
47 1384 AATGATGTCAAGCAGCTCATTAAGAAAGGAAGCACTCGAATCATGTGTCGACAGGGGT 1442
48
49 321 AsnAspAspLeuLeuPheSerIleAlaProGluValVal 333
50      :::::::::::::::::::::
51 1444 AATGAAGATATCATGATGATCAAGATGATTCGCCGAAGAAATT 1482
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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: ASCII
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/888,077A
/ FILING DATE: 03-JUL-1997
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/592,541
/ FILING DATE: 26-JAN-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: PALIST, THOMAS M
/ REGISTRATION NUMBER: 36,629
/ REFERENCE/DOCKET NUMBER: SCHERING 3.0-017 CIP CIP CIP IV
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (908) 654-5000
/ TELEFAX: (908) 654-7866
/ INFORMATION FOR SEQ ID NO: 41:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2205 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1..2205
/ OTHER INFORMATION: /note= "mctm1-TM2"
US-08-888-077A-41

Alignment Scores:
Pred. No.: 1,29e-110 Length: 2205
Score: 1034.50 Matches: 206
Best Similarity: 80.2% Conservative: 61
Best Local Similarity: 61.9% Mismatches: 57
Query Match: 61.6% Indels: 10
DB: Gaps: 2

US-10-617-443B-2 (1-334) x US-08-888-077A-41 (1-2205)
QY 4 A1aleuProlaSerlaGlyleuH1sg1nleuSerSerProArgrTyrlyPheanphe 23
DB 579 GGGAGCCCTGGCGCCAAAGGCGAG-GAAGATCCCAACAGTTTGGCCATTAATTAACCTTT 637
QY 24 1leaAaPValaValaGluys1lea1aProlaValaValaH1s1leg1leuPheuaArg 43
DB 638 ATCGCGGAGTGGTGAAGAAAGATCGCCCGCTGGTTCATATCGAATTTGGTTCGCAAG 697
QY 44 H1sProlaPheGlyArGaenValProlaSerSerGlySerGlyPhe1leuMetSerGlu 63
DB 698 CTTCCTTTTCTTAAACGAGAGGTGCGCGGTGCTGGCTGTTATTGTGTGGAA 757
QY 64 A1aGlyleu1le1leThraHn1aH1sVal1ValSerSerAanSer1a1a1aProlaArg 83
DB 758 GATGACTATCTGTGCAAAATGCGCACGTGTGACCAAC-----AAG 799
QY 84 G1nG1nleuValaG1nleuG1nAaenG1aSPSerTyrG1uA1aThrl1e1ySaP1le 103
DB 800 CACCGGCTCAAGTTAGCTGAAGAAAGCGGTGCCACTTACGAAGCAAAATCAAGATGCG 859
QY 104 AaPly1ySerSerP1lea1aThrl1e1yG1leH1sProlaYely1y1y1y1y1y1y1y 123
DB 860 GATGAAAGACGACACTCCACATCAAAATTGACCAAGGGGCAAGCTGCTGCTCG 919
QY 124 Leu1eug1yH1sSer1a1aPleuaArgProlaGly1yPheValaVala1leG1ySerPro 143
DB 920 CTGCTTGCGCGCTCTCAAGCTGCGCGGAGAGATGTGTGCTCCATCGGAAGCCCG 979
QY 144 PheA1a1eug1nAaenThraValThrl1y1leValaSerThra1a1a1a1a1a1a1a1a1a 163
DB 980 TTTTCCCTCAAAACACAGTCAACCAAGGATGTGAAGACCAACCAAGGAGGCGGCAAA 1039
QY 164 Glu1eug1y1euaArgaSPSerAaP1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y 183
DB 1040 GAGCTGGGCGCTCGCAATCAGACATGACATCAACGCAAGCCCATCACTAT 1099
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QY 184 GlyAaenSerGly1yProlaVala1aen1aenAaP1yG1uVala1leG1y1leAaenThrla 203
DB 1100 GGAACCTGGAGAGCGCCGTTAGTAACTGACGAGCGTGAAGCATTTGGAATTAACCTTTG 1159
QY 204 1ySVal1Thra1aG1y1leSerPheA1a1leProSeAaPArg1leThraArgPhe1eThr 223
DB 1160 AAAGTACAGCTGAATCTCTTTCGAATCCCATCTGAATTAAGATTAAGAAAGTTCTCCACG 1219
QY 224 GluPheG1nAaP1yG1n1le1yAaP-----T1y1y1y1y1y1y1y1y1y1y1y1y1y1y 240
DB 1220 GAGTCCCATGACCGACAGCCCAAGAAAGCCATCACCAAGAAAGATATATGTGTATC 1279
QY 241 ArgMeAaArgThrl1eThraProSerleuValaSPG1eul1yA1a1a1a1a1a1a1a1a1a 260
DB 1280 CGAATGATGTCACTCACTCACTCCAGCAAAAGCTGAAGAGACCGGACCGGACCTTC 1339
QY 261 ProG1uVala1SerSerGly1leTyrValaG1nG1uVala1aProlaenSerProSerG1nArg 280
DB 1340 CCAGACGTGATCTCAGAGCGGATATATTAATGAAGTAATTCCTGATATACCCAGCAAGACT 1399
QY 281 GlyGly1leG1nAaP1yAaP1le1leVala1ySVala1aenG1yAaP1yProlaValaAaSPer 300
DB 1400 GGTGTCTCAAGAAAGAAAGACGCTCATTAATCAAGCATCAATGACAGTCCGTGTCTCCGCC 1459
QY 301 SerG1u1eug1nG1uA1a1a1eul1eThrg1uSerProleu1eul1eG1uValaArgAArgGly 320
DB 1460 AATGATGTCAAGGAGAGCTCATTAAGAAAGAAAGCAACCTGAACATGTGTGTCCGAGGGGT 1519
QY 321 AaenAaP1eul1eThraPheSer1leA1aProlaG1uVala1 333
DB 1520 AATGAAGATATCATGATCAAGTGAATCCCAAGAAATTT 1558

RESULT 5
US-08-923-454A-17
/ Sequence 17, Application US/08923454A
/ Patent No. 6004794
/ GENERAL INFORMATION:
/ APPLICANT: Creasy, Caretha
/ APPLICANT: Livi, George
/ APPLICANT: Karren, Eric
/ APPLICANT: Clinkendear, Helen
/ APPLICANT: Browne, Michael
/ APPLICANT: Southan, Christopher
/ TITLE OF INVENTION: HUMAN SERINE PROTEASE
/ NUMBER OF SEQUENCES: 40
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: SmithKline Beecham Corporation
/ STREET: 709 Swedeland Road
/ CITY: King of Prussia
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19406
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/923,454A
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/025436
/ FILING DATE: 06-SEPT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Baumeister, Kirk
/ REGISTRATION NUMBER: 33,833
/ REFERENCE/DOCKET NUMBER: P50547
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 610-270-5096
/ TELEFAX: 610-270-5090
/ TELEX:
```

INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2036 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORIGINAL SOURCE: Feature polymorphism at 1325
US-08-923-454A-17

Alignment Scores:
Pred. No.: 7,496-110 Length: 2036
Score: 1027.50 Matches: 205
Percent Similarity: 79.94 Conservative: 61
Best Local Similarity: 61.64 Mismatches: 58
Query Match: 61.24 Indels: 10
DB: 3 Gaps: 2

US-10-617-443B-2 (1-334) x US-08-923-454A-17 (1-2036)

QY 4 AlaleuProAlaSerAlaGlyLeuH1eG1LeuSerSerProArgTyrLysPheAsnPhe 23
DB 503 GCGAGCCTTCGCGCCGCAAGGCGAG-GAAGATCCCAACAGTTGGCCCATATATATACCTT 561
QY 24 IleaAspValIvalGluLysIleAlaProAlaValIleAlaGluLeuPheLeuArg 43
DB 562 ATCCGGAGCGTGTGAGAGATGCGCCCTGCGGTTCATATGAAATGTTTGGCAAG 621
QY 44 HisProLeuPheGlyArgAsnValProLeuSerSerGlyPheIleMetSerGlu 63
DB 622 CTTCGTTTCTTAAACGAGAGGTGCGGTGCTAGTGGTTCGTTTATGTCGGA 681
QY 64 AlaGlyLeuIleIleThrAsnAlaHisValIleSerAsnSerAlaAlaProGlyArg 83
DB 682 GATGACTGATCGTACAAATGCGCCGAGGTGCGTGCATCGCAAC-----AAG 723
QY 84 GlnGlnLeuLysValGlnLeuGlnAsnGlyAspSerTyrGluAlaThrIleLysAspIle 103
DB 724 CACGGGTCCTCAAGTGAAGTGAAGACGATGCGCACTTCGAAAGCCAAATACAGATGCG 783
QY 104 AspLysLysSerAspIleAlaThrIleLysIleHisProLysLysLeuProValLeu 123
DB 784 GATGAAAGCAGCATCGCATCAAAATTGACACACAGGCGCAAGCTGCTGCTCG 843
QY 124 LeuLeuGlyHisSerAlaAspLeuArgProGlyGluPheValIleAlaGlySerPro 143
DB 844 CTGCTGGCCGCTCTCAAGCTGCGCGCGGAGAGTTGCTGTCGCCATCGGAAGCCCG 903
QY 144 PheAlaLeuGlnAsnThrValThrThrGlyIleValSerThrAlaGlnArgGluLysArg 163
DB 904 TTTTCCCTTCAAAACACAGTCCACCGGATCGTGAAGACACACAGGAGGCGGCAAA 963
QY 164 GluLeuGlyLeuArgAspSerAspMetAspTyrIleGlnThrAspAlaIleIleAsnTyr 183
DB 964 GAGCTGGGGCTCCGACATCGACATGAGTCAATCCAGACGAGCCCATCATCAATAT 1023
QY 184 GlyAsnSerGlyGlyProLeuValAsnLeuAspGlyGluValIleGlyIleAsnThrLeu 203
DB 1024 GGAACCTGGAGGCGCGCTTGTATTAACCTGAGCGGTGAAGTATGAAATTAAACCTTGG 1083
QY 204 LysValThrAlaGlyIleSerPheAlaIleProSerAspArgIleThrArgPheLeuThr 223
DB 1084 AAAGGACAGCTGGAATCTCTTTCATCCCATGTAAGATTAATAAAGTTCTCTCAG 1143
QY 224 GluPheGlnAspLysGlnIleLysAsp-----TrpLysLysArgPheIleGlyIle 240
DB 1144 GAGTCCCATGACGAGCCCAAGAAAGCCATCACCAAGAAAGATATTTGTATTC 1203
QY 241 ArgMetArgThrIleThrProSerLeuValAspGluLeuLysAlaSerAsnProAspPhe 260

DB 1204 CGAATGATGATCACCATCCAGCAACCAAGAGCTGAAGAGACCGGACCGGACTTC 1263
QY 261 ProGluValSerSerGlyIleTyrValGlnGluValAlaProAsnSerProSerGlnArg 280
DB 1264 CCAGACGATGATCCAGAGCGTATATATTAAGTAATTCCTGATACCCAGCAAGAACT 1323
QY 281 GlyGlyIleGlnAspGlyAspIleIleValLysValAsnGlyArgProLeuValAspSer 300
DB 1324 GKTGCTCAAGAAACGAGCATATATCATGATGAGACAGTCCGTGCTCCGCC 1383
QY 301 SerGluLeuGlnGluValLeuThrGluSerProLeuLeuGluValArgGlyIle 320
DB 1384 AATGATGACAGCAGCTCATTAATAAGGAAAGCACCCCTGAACATGCTGTCGAGGGGT 1443
QY 321 AsnAspAspLeuLeuPheSerIleAlaProGluValVal 333
DB 1444 AATGAAGTATCATGATCATCATGATTCCTCGAAGAAATT 1482

RESULT 6
US-09-724-864-22
Sequence 22, Application US/09724864
Patent No. 6380362
GENERAL INFORMATION:
APPLICANT: Watson, James D
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
FILE REFERENCE: 11000.1050U
CURRENT APPLICATION NUMBER: US/09/724,864
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 1859
TYPE: DNA
ORGANISM: Mouse
US-09-724-864-22

Alignment Scores:
Pred. No.: 2,436-97 Length: 1859
Score: 920.00 Matches: 191
Percent Similarity: 67.04 Conservative: 67
Best Local Similarity: 49.64 Mismatches: 66
Query Match: 54.84 Indels: 61
DB: 3 Gaps: 4

US-10-617-443B-2 (1-334) x US-09-724-864-22 (1-1859)

QY 4 AlaleuProAla-----SerAlaGlyLeuH1eG1Leu 14
DB 63 GCGCTCCCGCTGTGCGCAGTGCAGAGGGTCTGTCGAGAAAGCGGAGCAACAAAGACA 122
QY 15 SerSerProAlaGlyTyrLysPheAsnPheIleAlaAspValIleGluLysIleAlaProAla 34
DB 123 GGGCGGCTCCGAGAAAGATCACTTCGCGCAGGTGTGAGAAAGTGGCGCGCT 182
QY 35 ValValHisIleGluLeuPheLeuArg----- 43
DB 183 GTGTCCTTCAGAGCTGTTCCGAGATGACAGACACAGGTTCCCACTGATCTTAA 242
QY 43 ----- 43
DB 243 GAGAGACACCATCTGGAACCAAGATCTCAGTTGTTCGAAAGATGCGCCAGAGCA 302
QY 44 -----HisProLeuPheGlyArgAsnValPr 52
DB 303 GCTTCAGGACCTCAAAAGCAGATGAGATGATCACTTCCCAACGAAATCC 362
QY 52 OLeuSerSerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThrAsnAlaHis 72

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Db      363 TTCTCCAGCGGCTTGGGTTTCATAGTGTCTGAGAGATGGCTCATTTGTCACCAATGCCCA 422
QY      72  gvalvalserSeranSerAlaAlaProGlyArgGlnGlnLeuValGlnLeuGlnAs 92
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      423 COTCTCCACCAAC-----CACACGAAATCCAGGTAGAGCTCCAGAG 464
QY      92  nglValSerPyrGlnAlaThrIleValAspIleAspIleValSerAspIleAlaThrI 112
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      465 CCGGGCCCGGTTGTAAGCCACCGTCGAAAGACATGACATTAACCTGAGCCTTGACATGAT 524
QY      112 eluValIleHisProLysIleValLeuProValIleuLeuGlyHisSerAlaAspLeuAr 132
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      525 TTAAGATCGAGCCAGTACTGAGCTTCCAGTCTGCTGCTGGCCGATCTCTGACCTCCG 584
QY      132 gPrGlyGlnPheValAlaIleGlySerProPheAlaLeuGlnAlaThrValThrTh 152
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      585 GCGTGAAGATTGTGTGTTGCTTGGGAGCCCATTTCTCTGAGAAACACCGTGACTGC 644
QY      152 rGlyIleValSerThrAlaGlnArgGlnGluGlnLeuGlyLeuArgAspSerAspMe 172
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      645 AGGAGATTGTACACACACAGAGAGCGCGAGAGCTGGAGCTGAAAGATTCAGACAT 704
QY      172 tAspTyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyProLeuValAs 192
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      705 AGACTATATCCAGACGATCCATCTTAACATGAAATTCGGGGGTCCTCGGTGA 764
QY      192 nLeuAspGlyGlnValIleGlyIleAsnThrLeuValThrAlaGlyIleSerPheAl 212
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      765 CTTCGATGGCGACGATGTTGGTATTAACACTCTGAAGAGTACTGAGGAGATCTCTTTGC 824
QY      212 aIleProSerAspArgIleThrArgPheLeuThrGlnPheGlnAspLysGlnIleLys-- 231
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      825 GATCCCTCTGATGATTCAGACAGCTTCCTGGAAGACTCATGAGCGCGCATGTGAAG 884
QY      232 -----AspTrpLysIleValArgPheIleGlyIleArgMetArgThrIleProSer 249
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      885 CAAGGCCCTTGCAGAAATATCCTGGGCTTCGAAATGCTGCTCTCATCTGAACCT 944
QY      249 uValAspGlnLeuValAsnAsnProAspPheProGlnValIleSerGlyIleTyrVa 269
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      945 CCTTCAGAAATGAAGAGCGCAAGATCCAGAGTCCCTGATGTGAGTTCTGAGTTTGT 1004
QY      269 IGlInGlnValAlaProAsnSerProSerGlnArgGlyIleGlnAspGlyAspIleI 289
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1005 ATATGAAAGTATTCAGGATCGGCTCGCTGCAAGCTCGGGGTTGAGAGCATGATAT 1064
QY      289 eValIleValAsnGlyArgProLeuValAspSerSerGlnLeuGlnGlnValValLeuTh 309
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1065 TGTACACATTAACGGGCAACCTGTCAACCACTGATGTGATTAAGCA 1124
QY      309 rGlnSerProLeuLeuGlnValArgArgGlyValAsnAspAlaLeuLeuPheSerIleAl 329
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1125 CATGACTTCTCTCATCATGTGTCTGAGAGATCAACCTTTTCTGACAGCTCAC 1184
QY      329 aProGlnValVal 333
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1185 ACCTGAATATATC 1197

```

```

STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923.454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1835 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
AMT-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 251...1624
OTHER INFORMATION:
US-08-923-454A-7
Alignment Scores:
Pred. No.: 6,61e-93
Score: 882.00
Percent Similarity: 74.68
Best Local Similarity: 52.58
Query Match: 52.58
Gaps: 2
US-10-617-443b-2 (1-334) x US-08-923-454A-7 (1-1835)
QY      15 SerSerProArgTyrIlePheAsnPheIleAlaAspValAlaGlnValIleAlaProAla 34
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      671 GCTTCTCCCGGAGTGAAGTCACTTCGACGATGTGTGAGAGAAAGACGACCTGCC 730
QY      35  ValValHisIleIleGlnLeuPheLeuValArgHisProLeuPheGlnArgAsnValProLeuSer 54
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      731 GTGTCTATATTCAGATCCGACCGGACCTTTCTTGGGCGGAGGCTCTATCTCG 790
QY      55  SerGlySerGlyPheIleMetSerGlnValAlaGlyLeuIleIleThrAsnAlaHisValVal 74
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      791 AACGGCTCAGAGATTCTGGTGGCTCGGATGGCTCATTTGTCAACCAACCCCATGTGGTG 850
QY      75  SerSerAsnSerAlaAlaProGlyArgGlnGlnLeuValGlnLeuGlnAsnGlyAsp 94
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      851 GCTAT-----CGCGCAGAGTCCGTGTGAGACTGCTMAAGCGCGAC 892
QY      95  SerTyrGlnAlaThrIleValAspIleAspLysSerAspIleAlaThrIleLysIle 114
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      893 ACGTATGAGCGCGTGCACAGCTGTGATCCCGTGCACACATCCGACGCTGAGAGATT 952
QY      115 HisProLysIleValLeuProValIleuLeuGlyHisSerAlaAspLeuArgProGly 134

```



```

Db      953 CAGACTAAGAGACCTCTCCCAAGCTGCTGGAGACGTCAGTGTCCGGAAGG 1012
Qy      135 GtupheValAlaIleGlySerProPheAlaGluInAenThrValThrThyIle 154
Db      1013 GAGTTGTGTGTCATGGGAAGTCCCTTTCACATGCAAGAACATCATCCGGCATTT 1072
Qy      155 ValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuAAspSerAspMetAspTyr 174
Db      1073 GTTACCTCTGCTCAGACGTCACAGACCTGGAGATCCCAACCAATGTGAATAC 1132
Qy      175 IleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyProLeuValAsnLeuAsp 194
Db      1133 ATTCAAATGATGACGATTTGATTTTGAATCTGTGAGGTCCTCGTTAACTTGAT 1192
Qy      195 GlyGluValIleGlyIleAsnThrLeuValThraGlyIleSerPheAlaIlePro 214
Db      1193 GGGGAGGTGATGGATGAAACCATGAAGTCAAGCTGGAATCTCTTTCATCCCT 1252
Qy      215 SerAspArgIleThrArgPheLeuThrGluPheGlnAspGln-----Ile 230
Db      1253 TCTGATCGCTTCGAGAGTTCTGATCGTGGGAAAGAAATTCCTCTCCGGAATC 1312
Qy      231 LysAspTrpLysArgPheIleGlyIleArgMetArgThrIleThrProSerLeuVal 250
Db      1313 AGTGGGTCCCAAGCGGCGCTACATTTGGGTGATGATCTGACCTGATCCAGCATCTT 1372
Qy      251 AspGluLeuValAsnSerAsnProAspPheProGluValSerSerGlyIleTyrValGln 270
Db      1373 GCTGAATCAGACCTTCGAGAACCAAGCTTCCGATGTTCCAGCATGATGATCATCAT 1432
Qy      271 GluValAlaProAsnSerProSerGlnArgGlyIleGlnAspGlyAspIleIleVal 290
Db      1433 AAAGTCATCTGGGCTCCCTGACACCGGGCTGTCTGGGCTGGTGTGATGATTTTG 1492
Qy      291 LysValAsnGlyArgProLeuValAspSerSerGluLeuGlnAlaValLeuThrglu 310
Db      1493 GCCATTGGGAGCAATGTTACAAATGCTGAAGATGTTATGAAGCTTTGAAACCCA 1552
Qy      311 SerProLeuLeuGluValArgArgGlyAsnAspAspLeuLeuPheSerIleAlaPro 330
Db      1553 TCCCAATGAGCATGATCCGGGGGACGAGAAACACTGACCTTATATGTACCCCT 1612
Qy      331 GluVal 332
Db      1613 GAGGTC 1618

RESULT 8
US-09-075-460-4
; Sequence 4, Application US/09075460A
; Patent No. 6489136
; GENERAL INFORMATION:
; APPLICANT: Zervos, Antonio S.
; TITLE OF INVENTION: CELL PROLIFERATION RELATED GENES
; FILE REFERENCE: 10284/004001
; CURRENT APPLICATION NUMBER: US/09/075,460A
; CURRENT FILING DATE: 1998-05-08
; EARLIER APPLICATION NUMBER: US 60/046,077
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (248) ... (1834)
US-09-075-460-4

Alignment Scores:
Pred. No.: 7,77e-93 Length: 2040
Score: 882.00 Matches: 169

```

```

Percent Similarity: 74.8%
Best Local Similarity: 52.5%
Query Match: 52.5%
Db: 3 Gaps: 2
US-10-617-443b-2 (1-334) x US-09-075-460-4 (1-2040)

Qy      15 SerSerProArgTyrLysPheAsnPheIleAlaAspValAlaGluValIleAlaProAla 34
Db      881 GCTTCTCCCGAGTCAGTACACTTCACTCCAGATGTGGAGAAACACACACACTCTCC 940
Qy      35 ValValHisIleGluLeuPheLeuAAspProLeuPheGlyArgAsnValProLeuSer 54
Db      941 GTGGCTATATCGAGATCTGAGACCGGACCTTTCTTGGCCGGAGAGTCCATATCCG 1000
Qy      55 SerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThrAsnAlaHisValVal 74
Db      1001 AACGGCTCAGGATTCGTGTGGCTGCCATGGGCTCATTTGACCCACACCGCCATGTGTG 1060
Qy      75 SerSerAsnSerAlaAlaProGlyArgGlnGlnLeuValGlnLeuGlnAsnGlyAsp 94
Db      1061 GCTGAT-----CGGCGCAGAGTCCGTGTGAGACTCTTAAGCGGCAC 1102
Qy      95 SerTyrGluAlaIleIleGlySerProPheAlaGluInAenThrValThrThyIle 114
Db      1103 ACGTATAGGCGCGGTGTCACAGCTGTGATCCCGTGGCAGACATCGCAACGTCAGAT 1162
Qy      115 HisProLysLysLysLeuProValLeuLeuGlnGlyHisSerAlaAspLeuArgProGly 134
Db      1163 CAGACTAAGAGCCCTCTCCACGCTGCTGGGACCTCAGCTGATGTCCGGCAAGG 1222
Qy      135 GtupheValAlaIleGlySerProPheAlaGluInAenThrValThrThyIle 154
Db      1223 GAGTTGTGTGTCATGGGAAGTCCCTTTCACATGCAAGAACATCATCCGGCATTT 1282
Qy      155 ValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuAAspSerAspMetAspTyr 174
Db      1283 GTTACCTCTGCTCAGCGCTCCAGCCAGACGCTGGGACCTCCCAACCAAGTGAATAC 1342
Qy      175 IleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyProLeuValAsnLeuAsp 194
Db      1343 ATTCAAATGATGACGATTTGATTTGAAATCTTGAGAGTCCCTGTTAACTTGAT 1402
Qy      195 GlyGluValIleGlyIleAsnThrLeuValThraGlyIleSerPheAlaIlePro 214
Db      1403 GGGAGGTGATGGATGAAACCATGAAGTCAAGCTGAATCTCTTTCATCCCT 1462
Qy      215 SerAspArgIleThrArgPheLeuThrGluPheGlnAspGln-----Ile 230
Db      1463 TCTGATCGCTTCGAGAGTTCTGATCGTGGGAAAGAAATTCCTCTCCGGAATC 1522
Qy      231 LysAspTrpLysArgPheIleGlyIleArgMetArgThrIleThrProSerLeuVal 250
Db      1523 AGTGGGTCCCAAGCGGCGCTACATTTGGGTGATGATGCTGACCTGATGCCAGCATCTT 1582
Qy      251 AspGluLeuValAsnSerAsnProAspPheProGluValSerSerGlyIleTyrValGln 270
Db      1583 GCTGAATCAGACTTCGAGAACCAAGCTTCCAGATGTCAGCATGGTGTACTCATTCAT 1642
Qy      271 GluValAlaProAsnSerProSerGlnArgGlyIleGlnAspGlyAspIleIleVal 290
Db      1643 AAAGTCATCTGGGCTCCCTGACACACGGGCTGTCTCGCGCGTGTGATGATTTTG 1702
Qy      291 LysValAsnGlyArgProLeuValAspSerSerGluLeuGlnAlaValLeuThrglu 310
Db      1703 GCCATTGGGAGCAATGTTACAAATGCTGAAGATGTTATGAAGCTTTGAAACCCA 1762
Qy      311 SerProLeuLeuGluValArgArgGlyAsnAspAspLeuLeuPheSerIleAlaPro 330
Db      1763 TCCCAATGAGCATGATCCGGGGGACGAGAAACACTGACCTTATATGTACCCCT 1822
Qy      331 GluVal 332

```

DB 1823 GAGGTC 1828

RESULT 9

US-08-923-454A-23

Sequence 23, Application US/08923454A

Patent No. 6004794

GENERAL INFORMATION:

APPLICANT: Creasy, Caretha

APPLICANT: Livi, George

APPLICANT: Karian, Eric

APPLICANT: Clinkenbeard, Helen

APPLICANT: Souten, Christopher

TITLE OF INVENTION: HUMAN SERINE PROTEASE

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/923.454A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/025436

FILING DATE: 06-SEPT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Baumeister, Kirk

REGISTRATION NUMBER: 33,833

REFERENCE/DOCKET NUMBER: P50547

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-5096

TELEFAX: 610-270-5090

TELEX:

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 2187 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 603..1976

OTHER INFORMATION:

US-08-923-454A-23

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

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DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

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DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

Alignment Scores:

Pred. No.: 8.65e-93

Score: 882.00

Percent Similarity: 74.8%

Best Local Similarity: 52.5%

Query Match: 52.5%

DB: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-218

APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 2187 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHEetical: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 603...1976
OTHER INFORMATION:
US-08-923-454A-24
Alignment Scores:
Pred. No.: 8,65e-93 Length: 2187
Score: 882.00 Matches: 169
Percent Similarity: 74.8% Conservative: 72
Best Local Similarity: 52.5% Mismatches: 71
Query Match: 52.5% Indels: 10
DB: 3 Gaps: 2
US-10-617-443B-2 (1-334) x US-08-923-454A-24 (1-2187)
QY 15 SerSerProArgTyrIlyPhePheAnPheIleAlaAspValAlaGluIleValIleAlaProAla 34
DB 1023 GCTTCTCCCGGAGTCAGACAACTTCATCCGAGATGCTGAGAGACACACACTGCTGC 1082
QY 35 ValValHsiIleGluLeuPheLeuArgHisProLeuPheGlyArgAsnValProLeuSer 54
DB 1083 GTGGCTCTATATGAGATCCTGACCGGACCCCTTCTTGGGCGGAGGCTCCCTATCTCG 1142
QY 55 SerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThrAsnAlaHisValVal 74
DB 1143 AACGGCTTCGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1202
QY 75 SerSerAsnSerAlaAlaProGlyArgGlnGlnLeuValGlnLeuGlnAsnGlyAsp 94
DB 1203 GCTGAT-----CGGCGCAGAGTCCGCTGAGACTGCTAAGCGCGCAGC 1244

QY 95 SerTyrGluAlaThrIleIleAspIleAspIleAspIleAspIleAlaThrIleValIle 114
DB 1245 ACGTATGAGCCCGGTGTACAGCTGTGATCCCTGGCAGACATGCAACGCTGAGATT 1304
QY 115 HisProLysLysLysLeuProValLeuLeuLeuGlyHisSerAlaAspLeuArgProGly 134
DB 1305 CAGACTAAGAGAGCCCTCTCCACGCTGCTGGAGAGCTCAGCTGATGCTCGGCAAGG 1364
QY 135 GluPheValValAlaIleGlySerProPheAlaLeuGlnAsnThrValThrGlyIle 154
DB 1365 GAGTTGTGTTGGCATGGAAGTCCCTTGCACGTGCAAGACAGATCATCTCCGCAATT 1424
QY 155 ValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAspSerAspMetAspTyr 174
DB 1425 GTTAGCTCTGCTCAGCGCTCCAGCAGACCTGGAGACTCCCCCAACCAATGTGAATAC 1484
QY 175 IleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyProLeuValAsnLeuAsp 194
DB 1485 ATTCAACTGATGACGCTATGATTTGGAACCTTGAAGGTCCCTGTTAACCCTGAT 1544
QY 195 GlyLeuValIleGlyIleAsnThrLeuLysValThrAlaGlyIleSerPheAlaIlePro 214
DB 1545 GGGAGGTGATTGGAGTGAACACCATGAAGGTCAAGCTGGAATCTCTTGCATCCCT 1604
QY 215 SerAspArgIleThrArgPheLeuThrGluIleGlnAspLysGln-----Ile 230
DB 1605 TCTGATCTCTTCCAGAGCTTCTGATCTGATCTGGGAAAGAAATTCCTCTCCGGAATC 1664
QY 231 LysAspTyrLysArgPheIleGlyIleArgMetArgThrIleThrProSerLeuVal 250
DB 1665 AGTGGTCCCAAGCCGCTACATTTGGGTGATGATGTCGACCTGAGTCCAGCATCTCT 1724
QY 251 AspGluLeuLysAlaSerAsnProAspPheProGluValSerSerGlyIleTyrValGln 270
DB 1725 GCTGAACCTACAGCTTCAGAACCAAACTTCCGATGTCAGAGTGTACTCATTCAT 1784
QY 271 GluValAlaProAsnSerProSerGlnArgGlyIleGlnAspGlyAspIleIleVal 290
DB 1785 AAAGTCATCTGGGCTCCCTGCAACCCGCGCTGCTGCGCTGGTGAATGATTTTG 1844
QY 291 LysValAlaGlyArgProLeuValAspSerSerGluGlnAlaValLeuThrGlu 310
DB 1845 GCCATGGGAGCAGATGTCACAAATCTGAAGTGTATTGAAGCTTTCGAAACCA 1904
QY 311 SerProLeuLeuGluValAlaArgGlyLysAspAspLeuLeuPheSerIleAlaPro 330
DB 1905 TCCAGTTGGCAGTGCAGATCCGCGGGGAGCAGAAACACTGACCTTATGTGACCCCT 1964
QY 331 GluVal 332
DB 1965 GAGGTC 1970
RESULT 11
US-09-008-271A-23
Sequence 23, Application US/09008271A
Patent No. 6203979
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Hillman, Jennifer L.
Vue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SINCUCT01
CLONE: 2680548
SEQUENCE DESCRIPTION: SEQ ID NO: 23 :
US-09-008-271A-23

Alignment Scores:
Pred. No.: 1,05e-92 Length: 2476
Score: 882.00 Matches: 169
Percent Similarity: 74.8% Conservative: 72
Best Local Similarity: 52.5% Mismatches: 71
Query Match: 52.5% Indels: 10
DB: Gaps: 2

US-10-617-443B-2 (1-334) x US-09-008-271A-23 (1-2476)
QY 15 SerSerProAlaGlyTyrLeuPheAspPheIleAlaAspValAlaGluValIleAlaProAla 34
DB 481 GCTTCTCCCGAGTCAAGTCACTTCTCCAGATGTGTGGAGAGACGACCTGCC 540
QY 35 ValValHisIleGluLeuPheLeuArgHisProLeuPheGlyArgAsnValProLeuSer 54
DB 541 GTGGTCTATATGAGATCTCGACCGGACCTTTCTTGGCCCGGAGGTCCCTATCTCG 600
QY 55 SerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThrAsnAlaHisValVal 74
DB 601 AACGGCTCAAGATCTCTGGTGGCTGCCATGGGCTCATTTGTACCAAGCCCATGTGGTG 660
QY 75 SerSerAsnSerAlaIleProGlyArgGlnGlnLeuValGlnLeuGlnAsnGlyVal 94
DB 661 GCTGAT-----CGCGCAGAGTCCGTGTGAGACTGTAAAGCGGCAC 702
QY 95 SerTyrGluAlaThrIleLeuAspIleAspValSerAspIleAlaThrIleLeuVal 114
DB 703 ACCTATGAGGCGCTGTGTCAAGCTGTGATCCCGTGGCAGACATCCCAACGCTGAGATT 762
QY 115 HisProValSerLeuProValLeuLeuGluValHisSerAlaAspLeuArgProGly 134
DB 763 CAGACTRAGAGAGCTCTCCCGACGCTGCTGGACGCTGAGTATGTCCGGCAAGGG 822
QY 135 GluPheValAlaAlaIleGlySerProPheAlaLeuGlnAsnThrValThrThrGlyIle 154
DB 823 GAGTTTGTGTGCTGCAAGGAGAGCTTGTGCACTGAGACACATCATCTCCGCAAT 882
QY 155 ValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgSerAspMetAspTyr 174
DB 883 GTTAGCTGTGCTCAGCTCCAGCAGACGACTGGGACTCCCAACCAATGTGGAATAC 942

QY 175 IleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyProLeuValAsnLeuAsp 194
DB 943 ATTCAAACTGATGACGATGATGATTTTGGAACTCTGAGAGTCCCTGTTAACTGGAT 1002
QY 195 GlyGluValAlaIleGlyIleAsnThrLeuValThrAlaGlyIleSerPheAlaIlePro 214
DB 1003 GGGAGGTATTTGAGTGAACCATGAAAGTCACAGCTGAGATCTCTTGGCCATCCCT 1062
QY 215 SerAspArgIleThrArgPheLeuThrGluPheGlnAspIleValGln-----Ile 230
DB 1063 TCTGATCGCTTCTGAGAGTTTCTGCATCTGTGGGAAAGAAAGATTCCTCCCGGAATC 1122
QY 231 LysAspTyrPheLeuArgPheIleGlyIleArgMetArgThrIleThrProSerLeuVal 250
DB 1123 AGTGGTCCACGGCGGCTCAATGAGTGAATGCTACCTAGTCCGACATCTCT 1182
QY 251 AspGluLeuValAsnSerAspProAspPheProGluValSerSerGlyIleTyrValGln 270
DB 1183 GCTGAACCTACAGCTTCGAGAACCCAGCTTCCGATGTTCAAGCATGTCTACTCATCT 1242
QY 271 GluValAlaProAsnSerProSerGlnArgGlyIleGlnAspGlyAspIleIleVal 290
DB 1243 AAAGTCATCTCTGGGCTCCCTCGACACCGGGCTGTGCGGCTGTGATGTGATTTTG 1302
QY 291 LysValAsnGlyArgProLeuValAspSerSerGluGlnGluAlaValLeuThrGlu 310
DB 1303 GCATGTGGGAGCAGATGTACAAATGCTGAAGATGTTATGAACTGTTCAACACCA 1362
QY 311 SerProLeuLeuLeuGluValArgArgGlyAsnAspAspLeuPheSerIleAlaPro 330
DB 1363 TCCAGTTGGCAGTGCAGATCTCCGGCGGAGCAGAAACACTGACCTTATATGTGACCCCT 1422
QY 331 GluVal 332
DB 1423 GAGTTC 1428

RESULT 12
US-09-968-415-23
Sequence 23, Application US/09968415
Patent No. 6855811
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Hillman, Jennifer L.
Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purni
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Potter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,415
FILING DATE: 26-Sep-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/659,151
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SINVUCT01
CLONE: 2680548
SEQUENCE DESCRIPTION: SEQ ID NO: 23 :
US-09-968-415-23
Alignment Scores:
Pred. No.: 1,05e-92 Length: 2476
Score: 882.00 Matches: 169
Percent Similarity: 74.84 Conservative: 72
Best Local Similarity: 52.54 Mismatches: 71
Query Match: 52.54 Indels: 10
DB: 3 Gaps: 2
US-10-617-443B-2 (1-334) x US-09-968-415-23 (1-2476)
QY 15 SerSerProArgTyrLysPheAsnPhelIeAlaAspValaIgluYerIleAlaProAla 34
DB 481 GCTTCTCCCGAGTCAGTACAACTTTCATCGAGATGTGTGAGAAAGACAGACACTGCC 540
QY 35 ValValaHsiIleGluLeuPheLeuArgHsiProLeuPheGlyArgAsnValProLeuSer 54
DB 541 GTGGCTATATCGAGATCCTGGACCGGACCCCTTCTGGGCGCGAGGCTCCTATCTCG 600
QY 55 SerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThrAsnAlaHsiValaI 74
DB 601 AACGGCTAGAGATTGTGTGGTGGTCCGATGGCTCATTTGTCAACCAACCCCATGTGTG 660
QY 75 SerSerAsnSerAlaAlaProGlyArgGlnGluLeuValaGlnLeuGlnAsnGlyAsp 94
DB 661 GCTGAT-----CGGCCAGAGTCCGTGTAGACTGTGAAGCGGCAGC 702
QY 95 SerTyrGluAlaThrIleLysAspIleAspLysSerAspIleAlaThrIleLysIle 114
DB 703 ACGTATGAGCGCGGTGTCAAGCTGTGATCCGTTGGCAGACATCGCAACGCTGAGGATT 762
QY 115 HisProLysLysLeuProValLeuLeuLeuGlyHsiSerAlaAspLeuArgProGly 134
DB 763 CAGACTAAGAGACCTCTCCCAAGCTGCTCGGAGCGCTCAAGTGTCTCGGCAAGGG 822
QY 135 GluPheValaIleAlaIleGlySerProPheAlaLeuGlnAsnThrValThrThrGlyIle 154
DB 823 GAGTTTGTGTTCATGGAGAGTCCCTTTTGCATGCAACATCATCCGCGATT 882
QY 155 ValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAspSerAspMetAspTyr 174
DB 883 GTTACTCTGCTCAGCGTCCAGCAGAGACTGGGACTCCCAACCAAGATGTGAATAC 942
QY 175 IleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyProLeuValaAsnLeuAsp 194
DB 943 ATTCAACTGAGAGCTATTGATTTTGGAACTGTGAGAGTCCCTGTGTAACCTGAT 1002
QY 195 GlyGluValaIleGlyIleAsnThrLeuLysValThrAlaGlyIleSerPheAlaIlePro 214
DB 1003 GGGAGGAGTATGGAGTGAACCATGAAAGGTCAAGCTGGAAATCTCTTTCATCCCT 1062
QY 215 SerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGln-----Ile 230
DB 1063 TCTGATCGCTTCGAGAGATTCTGCATCGTGGGAAAGAAAGAAATTCCTCCGGAATC 1122
QY 231 LysAspTyrLysLysArgPheIleGlyIleArgMetArgThrIleThrProSerLeuVal 250
DB 1123 AGTGGTCCCAAGCGCGCTACATTTGGGGTGATGATGATCCCTGAGTCCCGACATCTCT 1182
QY 251 AspGluLeuLysAlaSerAsnProAspPheProGluValaSerSerGlyIleTyrValGln 270

DB 1183 GCTGAACATACAGCTTCGAGAACCAAGCTTCCCATGTTTCAGCATGTGTACTATCCAT 1242
QY 271 GluValaIleProAsnSerProSerGlnArgGlyIleGlnAspGlyAspIleIleVal 290
DB 1243 AAAGTCATCTGGGCTCCCTCCCTGACACCGGGCTGTGCGGCTGTGATGTGATTTTG 1302
QY 291 LysValaGlnArgProLeuValaAspSerSerGluLeuGlnGluValaValLeuThrGlu 310
DB 1303 GCCATTGGGAGACGATGTATCAAAATCTGAAGATGTTTATGAAGCTGTTCGAACCCA 1362
QY 311 SerProLeuLeuGluValaArgArgLysAsnAspLeuLeuPheSerIleAlaPro 330
DB 1363 TCCAGTTGGCAGTCGACATCCGCGGAGACGAGAAACATGACTTATATGTACCCCT 1422
QY 331 GluVal 332
DB 1423 GAGTTC 1428
RESULT 13
US-08-923-454A-30
Sequence 30, Application US/08923454A
Patent No. 6004794
GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Livi, George
APPLICANT: Karren, Eric
APPLICANT: Clinkendard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSER: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Pasteo Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 2187 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE: Polymorphic variants at 672 and 1435
FEATURE: aa24=Arg/Cys aa278=Ala/Val
NAME/KEY: Coding Sequence

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LOCATION: 603...1976
OTHER INFORMATION:
US-08-923-454A-30

Alignment Scores:
Pred. No.: 2,54e-92      Length: 2187
Score: 878.00           Matches: 168
Percent Similarity: 74.5%      Conservative: 72
Best Local Similarity: 52.2%    Mismatches: 72
Query Match: 52.3%           Indels: 10
DB: 3                      Gaps: 2

US-10-617-443B-2 (1-334) x US-08-923-454A-30 (1-2187)

QY 15 SerSerProArgTyrIlePheAsnPhelIeAlaAspValaIGluYsileAlaProAla 34
DB 1023 GCTTCTCCCGGAGTACAGTCACTTCGACAGATGTGTGGAGAAAGACACACCTGCC 1082
QY 35 ValValHleIleGluPheLeuArgHlsProLeuPheGlyArgAsnValProLeuSer 54
DB 1083 GTGGTCTATATGAGATCCTGACCGGACCCCTTCTTGGCGCGGAGGTCTCTATCTG 1142
QY 55 SerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThrAsnAlaHisVala 74
DB 1143 AACGGCTCAGGATTCGTGTGGCTGCCGATGGGCTCATGTGTCCACACCGCCATGTGTG 1202
QY 75 SerSerAsnSerAlaAlaProGlyArgGlnGlnLeuValGlnLeuGlnAsnGlyAsp 94
DB 1203 GCTGAT-----CGGCGCAGAGTCGCTGTGAGACTGCAAGCGCGCAGC 1244
QY 95 SerTyrGluAlaThrIleIleYsAspIleAspYsSerAspIleAlaThrIleYsile 114
DB 1245 ACCTATGAGGCCCTGTGGCAGCTGATCCGTGGCAGACATCGACAGCTGAGGATT 1304
QY 115 HisProYsYsYsLeuPheProValLeuLeuGlyHisSerAlaAspLeuArgProGly 134
DB 1305 CAGACTRAGAGGCTCTCCCGACGCTGCTCTGGGACGCTGACATGTCTCGGCAAGGG 1364
QY 135 GluPheValaValaIleGlySerProPheAlaLeuGlnAsnThrValThrThrGlyIle 154
DB 1365 GAGTTTGTGTGTCATGAGGAAAGTCCCTTGTGACCTGCAAGAACAGATCAGATCCGGCATT 1424
QY 155 ValSerThrAlaGlnArgGluGlyArgGlnLeuGlyLeuArgAspSerAspMetAspTyr 174
DB 1425 GTTAGCTCTCTCGGCTCCAGCCAGACCTGGGACTCCCGCCAAACATGTGGAAATAC 1484
QY 175 IleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyProLeuValAsnLeuAsp 194
DB 1485 ATTCAAACTGATGACGATATTGATTGGAAACTCTGAGAGTCCCTGTTAACCTGGAT 1544
QY 195 GlyGluValaIleGlyIleAsnThrLeuYsValThrAlaGlyIleSerPheAlaIlePro 214
DB 1545 GGGAGGTGATGGAGTGAACACATGAAGTCAAGCTGAATCTCTTGTCCATCTCT 1604
QY 215 SerAspArgIleThrArgPheLeuThrGlnPheGlnAspYsGln-----Ile 230
DB 1605 TCTATGCTCTTCGAGACTTCTCTGCATGTGGGAAAAGAAAGAAATTCCTCTCCGGAATC 1664
QY 231 LysAspTyrIleYsYsArgPheIleGlyIleArgPheArgThrIleThrProSerLeuVal 250
DB 1665 AGTGGGTCCAGCGCGCTCATATTGGGGTGTGATGTGACCTCGAGTCCGAGCATCTCT 1724
QY 251 AspGluLeuYsAlaSerAsnProAspPheProGluValaSerSerGlyIleTyrValGln 270
DB 1725 GCTGAACATACAGCTTCGAAACCAAGCTTTCCTCCATGTTCAGCATGTGTACTCATCAT 1784
QY 271 GluValaIleProAsnSerProSerGlnArgGlyIleGlnAspGlyAspIleIleVal 290
DB 1785 AAAGTCATCCCGGGCTCCCTGCAACACCGGCTGGTGTGCGGCGCTGTGATGTGATTTG 1844
QY 291 LysValaIleGlyArgProLeuValaAspSerSerGluLeuGlnGluValaValLeuThrGlu 310
DB 1845 GCCATTGGGAGCAGATGTGTAACAAATGCTGAAGATGTTTATGAAGCTGTTTGAACCCAA 1904

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QY 311 SerProLeuLeuGluValaIleArgGlyAsnAspAspLeuPheSerIleAlaPro 330
DB 1905 TCCAGTTGGCAGATCCGCGGGGAGAGAAACACTGACCTTATATGTGACCCCT 1964
QY 331 GluValaI 332
DB 1965 GAGGTTC 1970

RESULT 14
US-08-923-454A-3
Sequence 3, Application US/08923454A
Patent No. 6004794
GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Livi, George
APPLICANT: Kairan, Eric
APPLICANT: Clinkenbeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESS: Smithline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1787 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-923-454A-3

Alignment Scores:
Pred. No.: 2,27e-87      Length: 1787
Score: 834.50           Matches: 169
Percent Similarity: 60.7%      Conservative: 72
Best Local Similarity: 42.6%    Mismatches: 71
Query Match: 49.7%           Indels: 85
DB: 3                      Gaps: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-3 (1-1787)

QY 15 SerSerProArgTyrIlePheAsnPhelIeAlaAspValaIGluYsileAlaProAla 34

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Db 259 GCTTCTCCCGAGTCAGTACACTTCATCGCAGATGTGTGAGAGAAAGCAGCCTCC 318
Qy 35 ValValHisIleGluLeuPheLeuArgHisProLeuPheGlyArgAsnValProLeuSer 54
Db 319 GTGGCTTATTCAGATCTCGAAGCGGACCTCTTCTTGGGCGGAGAGTCCCTATCTCG 378
Qy 55 SerGlySerGlyPheIleMetSerGluIleGlyLeuIleIleThrAsnAlaHisValVal 74
Db 379 AACGGCTCAGATTCGTGTGCTGCCATCGGCTCATGTGCACCAAGCCCATGTGGTG 438
Qy 75 SerSerAsnSerAlaAlaProGlyArgGlnLeuLeuValGlnLeuGlnAsnGlyAsp 94
Db 439 GCTGAT-----CGGCGCAGAGTCCGTGTGAGACTGTGAAGCGGCGAC 480
Qy 95 SerTyrgluAlaThrIleLeuAspIleAspIleAspIleAspIleAlaThrIleAspIle 114
Db 481 ACGTATGAGCGCGTGTGACAGCTGTGATCCGTCGACAGCATCGCAACGCTGAGATT 540
Qy 115 HisProLysLysLeuProValLeuLeuGluGlnHisSerAlaAspLeuAspProGly 134
Db 541 CAGACTTAAAGACCTCTCCCAAGCTGCTGTGAGCGCTCATGATGTCCGCGAAGG 600
Qy 135 GluPheValValAlaIleGlySerProPheAlaLeuGlnAsnThrValThrGlyIle 154
Db 601 GAGTTTGTGTTCATGAGGAAGTCCCTTTCAGCTGACGAGAACAGATCATCATCCGCGATT 660
Qy 155 ValSerThrAlaGlnArgGluGlyArgGluLeuGluLeuArgSerAspMetAspTyr 174
Db 661 GTTAGCTCTGCTCAGCGCTCAGCGCAGACCTGGGACCTCCCAACCAATGTGAATAC 720
Qy 175 IleGlnThrAspAlaIleIleAsnTyrglyAsnSerGlyIleProLeuValAsnLeu 193
Db 721 ATTCAACTGATGAGCTATTGATTTGTGAACCTGAGAGGCTCCCTGTATTAACCTGGTG 780
Qy 193 ----- 193
Db 781 AGTGAACATCTTCCTTCCAAGATCCCTGCCAGGTGAGTGGGAAGGTAGTTT 840
Qy 193 ----- 193
Db 841 CCCCTAATTCAAGATGTTTGTGCAAGTTCGACAGATTCCTTGTGGCTATCTCTCA 900
Qy 193 ----- 193
Db 901 TATCAACACAGATCTCCCAACACTTGTCTGACTTTTGTGGGTGCCCATCCCTA 960
Qy 194 ----- 194
Db 961 CTATTGTTTAAAGGCTAAGGAACTGGGGGCTGATCCCTGACAGATGGGGAAGTATGGA 1020
Qy 200 IleAsnThrLeuLysValIleThrAlaGlyIleSerPheAlaIleProSerAspArgIleThr 219
Db 1021 GTGAACACCATGAAGGTCAAGCTGGAATCTCTTGCATCCCTTGCATGCTGCTTGA 1080
Qy 220 ArgPheLeuThrGluPheGlnAspIleGln-----IleLysAspTyrLys 235
Db 1081 GAGTTCTGCACTCGTGGGAAAGAAAGAAATTCCTCCGGAATCAGTGGGTCCGAGGG 1140
Qy 236 ArgPheIleGlyIleArgMetArgThrIleThrProSerLeuValAspGluLeuLysAla 255
Db 1141 CGCTACATTTGGGGTATGATCTGACCTGAGTCCCAACATCCTTGCAGACTACAGCTT 1200
Qy 256 SerAsnProAspPheProGluValSerSerGlyIleTyrgluGlnGluValAlaProAsn 275
Db 1201 CGAGAACCAACCTTCCGATGTTTCAGCATGTGTGACTCATCAATAAGTCACTCTGGGC 1260
Qy 276 SerProSerGlnArgGlyGlyIleGlnAspGlyAspIleIleValLysValAsnGlyArg 295
Db 1261 TCCCTGACACCGGGCTGTGCTGCGGCTGTGATGATTTTGGCCATTGGGAGAGAG 1320
Qy 296 ProLeuValAspSerSerGluLeuGlnGluValValLeuThrGluSerProLeuLeu 315

Db 1321 ATGGTACAAATGCTGAGATGTTATGAGACTGTTGCAACCCATCCAGTTGGCAGTG 1380
Qy 316 GluValAlaArgArgGlyAsnAspAspLeuLeuPheSerIleAlaProGluVal 332
Db 1381 CAGATCCGCGCGGAGCAGAAACACTGACTTATATGTGACCCCTGAGGTC 1431
RESULT 15
US-08-923-454A-26
Sequence 26, Application US/08923454A
Patent No. 6004794
GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Livl, George
APPLICANT: Karan, Eric
APPLICANT: Clinkenbeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: NO
ORIGINAL SOURCE:
FEATURES:
NAME/KEY: Coding Sequence
LOCATION: 603..1733
OTHER INFORMATION:
US-08-923-454A-26
Alignment Scores:
Pred. No.: 3,93e-87 Length: 2551
Score: 834.50 Matches: 169
Percent Similarity: 60.7% Conserves: 72
Best Local Similarity: 42.6% Mismatches: 71
Query Match: 49.7% Indels: 85
DB: 3 Gaps: 3
US-10-617-443B-2 (1-334) x US-08-923-454A-26 (1-2551)

[illegible]

Db 2085 ATGCTACAAATGCTGAAGATGTTATGACCTTTGCAACCCATCCCATGTTGGCAGTG 2144
 GY 316 GIVATAlArGArGlyAsmAspAspLeuPheSerIleAlaProGluVal 332
 Db 2145 CAGATCCGGCGGGGCGAGAAACACTGACCTTATATGTGACCCCTGAGGTC 2195

Search completed: February 21, 2006, 20:37:03
Job time : 231 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceeleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 21, 2006, 20:37:21 Search time 823 Seconds

(without alignments)
3355.981 Million cell updates/sec

Title: US-10-617-443B-2

Perfect score: 1679
Sequence: 1 MHLALPASAGHQLSSPRK.....LEVRGNDDLFLSTAPEVVM 334

Scoring table:

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Xgapop 10.0, Xgapext 0.5	
Ygapop 10.0, Ygapext 0.5	
Fgapop 6.0, Fgapext 7.0	
Delop 6.0, Delext 7.0	

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-MINMATCH=0.1-LOOPEXT=0-LOOPEXT=0-LISTS=bits-START=1-END=1
-MATRIX=blosum62-TRANS=human40.cdi-LIST=45-DOCCALIGN=200-THR_SCORE=pct
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-HEADSIE=500-MINLEN=0-MAXLEN=200000000-HOST=abs03p
-USER=US10617443@CGN 1.1.1549@runat.21022006.165828.17349-NCPU=6-ICPU=3
-NO_MMAP-NEG_SCORES=0-WAIT-DSPBLOCK=100-LOGLOG-DEV_TIMEOUT=120
-WARN_TIMEOUT=30-THREADS=1-XGAPOP=10-XGAPEXT=0.5-FGAPOP=6-FGAPEXT=7
-YGAOP=10-YGAPEXT=0.5-DELOP=6-DELEXT=7

Database: Published.Applications.NA.Main:

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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1679	100.0	3006	6	US-10-189-099A-1
2	1679	100.0	3006	8	US-10-617-443B-1
3	1635	97.4	1044	3	US-09-796-858-9
4	1635	97.4	1563	3	US-09-796-753-33
5	1635	97.4	1797	7	US-10-275-505-28
6	1635	97.4	1797	10	US-11-140-224-28
7	1635	97.4	2040	3	US-09-818-143-14

8	1635	97.4	2094	7	US-10-381-820A-7	Sequence 7, Appl1
9	1635	97.4	2541	9	US-10-956-157-5181	Sequence 5181, Ap
10	1635	97.4	2543	9	US-10-485-313A-31	Sequence 31, Appl
11	1635	97.4	2576	3	US-09-796-753-31	Sequence 31, Appl
12	1536	91.5	2450	9	US-10-485-313A-26	Sequence 26, Appl
13	1482.5	88.3	2551	6	US-10-301-822-78	Sequence 78, Appl
14	1378	82.1	1868	3	US-09-764-898-112	Sequence 112, App
15	1122	66.8	1695	3	US-09-969-384-7	Sequence 7, Appl1
16	1117	66.5	1953	9	US-10-485-313A-32	Sequence 32, Appl
17	1105	65.8	1788	3	US-09-764-898-40	Sequence 40, Appl
18	1057	63.0	1897	9	US-10-485-313A-38	Sequence 38, Appl
19	1034.5	61.6	1440	3	US-09-796-858-7	Sequence 7, Appl1
20	1034.5	61.6	1894	6	US-10-104-047-795	Sequence 795, App
21	1034.5	61.6	2034	3	US-10-102-524-1732	Sequence 1732, Ap
22	1034.5	61.6	2036	3	US-09-960-706-516	Sequence 516, App
23	1034.5	61.6	2036	6	US-10-170-385-356	Sequence 356, App
24	1034.5	61.6	2036	6	US-10-17-118-815	Sequence 815, App
25	1034.5	61.6	2036	6	US-10-342-887-815	Sequence 815, App
26	1034.5	61.6	2036	8	US-10-772-636-47	Sequence 47, Appl
27	1034.5	61.6	2036	9	US-10-956-157-919	Sequence 919, App
28	1034.5	61.6	2054	5	US-10-084-817-32	Sequence 32, Appl
29	1034.5	61.6	2437	5	US-10-198-846-10826	Sequence 10826, A
30	1027.5	61.2	2157	6	US-10-264-049-135	Sequence 135, App
31	1006.5	59.9	1855	3	US-09-925-298-134	Sequence 134, App
32	1006.5	59.9	1855	5	US-10-102-806-134	Sequence 134, App
33	1005.5	59.9	2212	8	US-10-723-860-5299	Sequence 5299, Ap
34	981.5	58.5	1534	3	US-09-765-221A-20	Sequence 20, Appl
35	945	56.3	1328	9	US-10-764-420-1506	Sequence 1506, Ap
36	920	54.8	1859	5	US-09-866-050A-588	Sequence 588, App
37	920	54.8	1859	5	US-10-152-661-588	Sequence 588, App
38	890	53.0	1544	8	US-10-789-241-49	Sequence 49, Appl
39	890	53.0	1544	8	US-10-772-636-7	Sequence 7, Appl1
40	890	53.0	1553	3	US-09-935-390A-18	Sequence 18, Appl
41	882	52.5	963	7	US-10-730-476A-11	Sequence 11, Appl
42	882	52.5	963	9	US-10-730-476A-11	Sequence 11, Appl
43	882	52.5	975	7	US-10-730-476A-1	Sequence 1, Appl1
44	882	52.5	975	9	US-10-730-476A-1	Sequence 1, Appl1
45	882	52.5	1374	5	US-10-197-634-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-10-189-099A-1
; Sequence 1, Application US/10189099A
; Publication No. US20040005659A1

GENERAL INFORMATION:

APPLICANT: Darrow, Andrew L
APPLICANT: Qi, Jjian-shen
APPLICANT: Chen, Callin
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Human PRSS-11 like S2 serine protease and uses thereof
FILE REFERENCE: ORT-1644
CURRENT APPLICATION NUMBER: US/10/189, 099A
CURRENT FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 3006
TYPE: CDNA
ORGANISM: Homo sapiens
US-10-189-099A-1

Alignment Scores:

Pred. No.:	3,93e-180	Length:	3006
Score:	1679.00	Matches:	334
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatch:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-617-443B-2 (1-334) x US-10-189-099A-1 (1-3006)

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Qy      21 PheAsnPhelIeAlaAspValValGluYsiIeAlaProAlaValAlaHisiGlnLeu 40
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Qy      41 PheLeuArgHisProLeuPheGlyArgAsnValProLeuSerSerGlySerGlyPheIle 60
      |||
      1131 TTCCTGAGACACCGCGCTGTGGCCGACGTCGCCCTGTCCAGCGGTTCCTTGCCTTCATC 1190
Qy      61 MetSerGluAlaGlyLeuIleIleThrAsnAlaHisiValAlaSerSerAsnSerAlaAla 80
      |||
      1191 ATGTCAGAGGCCCGCCCTGATCATCCCAATGCCACCTGCTGTCCAGCAACATGCTGCC 1250
Qy      81 ProGlyArgGlnGlnLeuLysValGlnLeuGlnAsnGlyAspSerTyrGluAlaThrIle 100
      |||
      1251 CCGGGCAGCGCAGCAGCTCAAGTGCAGCTACAGAAATGGGAGCTCTTATAGGCGCACCATC 1310
Qy      101 LysAspIleAspLysSerAspIleAlaThrIleYsiIeHisProLysLysLeu 120
      |||
      1311 AAAGACATTCACAAAGATCGACATTGCCACATCAAGATCCATCCCAAGAAAAGCTC 1370
Qy      121 ProValLeuLeuLeuGlyHisSerAlaAspLeuArgProGlyGluPheValValAlaIle 140
      |||
      1371 CCGTGTGTGTGCTGGGTCACTGGCGGACCTGGCGCTGGGAGTTGTGTGGTGCATC 1430
Qy      141 GlySerProPheAlaLeuGlnAsnThrValThrThrGlyIleValSerThrAlaGlnArg 160
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      1431 GGCAGTCCCTTCCGCCCTACAGAACACAGTACAAACGGGCACTGTCAGACTGCCAGCGG 1490
Qy      161 GluGlyArgGluLeuGlyLeuArgAspSerAspMetAspTyrIleGlnThrAspAlaIle 180
      |||
      1491 GAAGGCGAGGAGCTGGGCTCCCGAGCTCCGACATGACATCAAGAGATGACATC 1550
Qy      181 IleAsnTyrGlyAsnSerGlyGlyProLeuValAsnLeuAspGlyGluValIleGlyIle 200
      |||
      1551 ATCACTACAGGGAACCTCGGGGGAACCACTGTGTGATGCTGATGCGAGGCTTGGCATC 1610
Qy      201 AsnThrLeuLysValThrAlaGlyIleSerPheAlaIleProSerAspArgIleThrArg 220
      |||
      1611 AACACCTCAAGGTTCACGCTGCGCATCTCTTGGCCATCCCTTCAGACCGCATCACACG 1670
Qy      221 PheLeuThrGluPheGlnAspLysGlnIleLysAspTyrLysAspPheIleGlyIle 240
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      1671 TTCCTCAAGAGTTCCAGACAGCAGATCAAGATCAAGAGCGCTTCATCGGCATTA 1730
Qy      241 ArgMetArgThrIleThrProSerLeuValAspGluLeuLysAsnProAspPhe 260
      |||
      1731 CGGATCGGAGCATCACCAACCTGTGTGATGAGCTGAGGCGCAACCCGGACTTC 1790
Qy      261 ProGluValSerSerGlyIleYrValGlnGluValAlaProAsnSerProSerGlnArg 280
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Qy      281 GlyGlyIleGlnAspGlyAspIleIleValLysValAsnGlyArgProLeuValAspSer 300
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      1851 GGGCGCATTCCAAGATGATGATCATCATGCTCAAGGTCACGGCGCTCTCTAGTGAATCG 1910
Qy      301 SerGluLeuGlnGlnAlaValLeuThrGluSerProLeuLeuLeuGluValAlaArgArgGly 320
      |||
      1911 AGTGAAGCTGACAGAGCGCGTGCATCGACGAGTCTCTCTCTTACTGAGAGGTGGCGGGG 1970
Qy      321 AsnAspAspLeuLeuPheSerIleAlaProGluValAlaMet 334
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      1971 AAGACGACCTCTCTTCAAGCATCGACCTGAGGTGATCATG 2012

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RESULT 2
US-10-617-443B-1
; Sequence 1, Application US/10617443B
; Publication No. US2005001977A1
; GENERAL INFORMATION:

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; APPLICANT: Darrow, Andrew L
; APPLICANT: Qi, Jian-shen
; APPLICANT: Chen, Caifan
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Human PRSS-11 like S2 serine protease and uses thereof
; FILE REFERENCE: ORT-1644
; CURRENT APPLICATION NUMBER: US/10/617,443B
; CURRENT FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3006
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-617-443B-1

Alignment Scores:
Pred. No.: 3,93e-180 Length: 3006
Score: 1679.00 Matches: 334
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-617-443B-2 (1-334) x US-10-617-443B-1 (1-3006)

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Qy      101 LysAspIleAspLysSerAspIleAlaThrIleYsiIeHisProLysLysLeu 120
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Qy      121 ProValLeuLeuLeuGlyHisSerAlaAspLeuArgProGlyGluPheValValAlaIle 140
      |||
      1371 CCGTGTGTGTGCTGGGTCACTGGCGGACCTGGCGCTGGGAGTTGTGTGGTGCATC 1430
Qy      141 GlySerProPheAlaLeuGlnAsnThrValThrThrGlyIleValSerThrAlaGlnArg 160
      |||
      1431 GGCAGTCCCTTCCGCCCTACAGAACACAGTACAAACGGGCACTGTCAGACTGCCAGCGG 1490
Qy      161 GluGlyArgGluLeuGlyLeuArgAspSerAspMetAspTyrIleGlnThrAspAlaIle 180
      |||
      1491 GAAGGCGAGGAGCTGGGCTCCCGAGCTCCGACATGACATCAAGATCCCAAGAGATGCTC 1550
Qy      181 IleAsnTyrGlyAsnSerGlyGlyProLeuValAsnLeuAspGlyGluValIleGlyIle 200
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Qy      201 AsnThrLeuLysValThrAlaGlyIleSerPheAlaIleProSerAspArgIleThrArg 220
      |||
      1611 AAGACGCTCAAGGTTCAGCGGTGCATCTCTTGGCATCCCTTCAGACCGCATCACACG 1670
Qy      221 PheLeuThrGluPheGlnAspLysGlnIleLysAspTyrLysAspPheIleGlyIle 240
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      1671 TTCCTCAAGAGTTCCAGACAGCAGATCAAGATCAAGAGCGCTTCATCGGCATTA 1730

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QY 241 ArgMetArgThrIleTherProSerLeuValaAspGluLeuValaSerAsnProAspPhe 260
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QY 261 ProGluValSerSerGlyIleTyValGlnGluValaAlaProAsnSerProSerGlnArg 280
Db 1791 CCAGAGGTGACAGAGGGAATTTATGTGCAAGAGGTGGCCGAATTCACCTTCTCAGAGA 1850
QY 281 GlyIleIleGlnAspGlyAspIleIleVallyValaAsnGlyArgProLeuValaAspSer 300
Db 1851 GCGCGCATTCAGAGAGGTGACATTCGTCAGAGTCACAGGCGCTCTTACTGACACTCG 1910
QY 301 SerGluLeuGlnGluAlaValLeuThrGluSerProLeuLeuGluValaArgArgGly 320
Db 1911 AGTGAGTGTCCAGAGAGCGGTGCTGACCGAGTCTCTCTCTAAGAGGTGCGGCGGCG 1970
QY 321 AsnAspAspLeuLeuPheSerIleAlaProGluValaMet 334
Db 1971 AACGACGACCTCTCTTCCAGCATCCGACCTGAGGTGTCATG 2012

RESULT 3

US-09-796-858-9
; Sequence 9, Application US/09796858
; Patent No. US20020055139A1

GENERAL INFORMATION:

APPLICANT: Holteiman, Douglas
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING PROGNOSTIC, DIAGNOSTIC,
FILE REFERENCE: PREVENTIVE, THERAPEUTIC, AND OTHER USES
CURRENT FILING DATE: 7853-226-999
CURRENT FILING DATE: US/09/796, 858
PRIOR APPLICATION NUMBER: 09/223, 094
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/223, 546
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/224, 246
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/312, 359
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/336, 536
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 09/342, 687
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 09/399, 723
PRIOR FILING DATE: 1999-09-20
PRIOR APPLICATION NUMBER: 09/471, 179
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 09/474, 071
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/474, 072
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/572, 002
PRIOR FILING DATE: 2000-05-14
PRIOR APPLICATION NUMBER: 09/597, 993
PRIOR FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: 09/599, 596
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/606, 565
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/665, 164
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 09/630, 334
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 09/665, 666
PRIOR FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 50
SEQ ID NO 9
LENGTH: 1044
TYPE: DNA
ORGANISM: Mouse
US-09-796-858-9

Alignment Scores:

Pred. No.: 8-75e-176 Length: 1044
Score: 1635.00 Matches: 325
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 3 Gaps: 0

US-10-617-443B-2 (1-334) x US-09-796-858-9 (1-1044)

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Db 130 AAGATCGACCAAGCGGTGTCCACATAGAGCTCTTCCGAGACACCCCTGTTGGCGCG 189
QY 50 AsnValProLeuSerSerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThr 69
Db 190 AACGTGCCCCCTGTCCAGCGGTTCGTGCTTCATCATGTCAAGGCGGCGCTGATCATCAC 249
QY 70 AsnAlaHisValaSerSerAsnSerAlaAlaProGlyArgGlnGlnLeuValaGln 89
Db 250 AATGCCCAAGTGTGTCCAGCAACAGTCTGCCCCGAGGACAGCAAGTGCAG 309
QY 90 LeuGlnAsnGlyAspSerTyrGluAlaThrIleLysAspIleAspLysSerAspIle 109
Db 310 CTACAGAAATGGGGACCTCTTAAGAGGCCACATCAAGACATCGACAMAGTCGACATT 369
QY 110 AlaThrIleLysIleHisProLysLysLysLeuProValaLeuLeuGlyHisSerAla 129
Db 370 GCGACCATCAAGATTCATCCAGAAAGCTCCCTGTGTGTCTGAGTCACTCGGCC 429
QY 130 AspLeuArgProGlyGluPheValaValaIleGlySerProPheAlaLeuGlnAsnThr 149
Db 430 GACCTGGCGGCTGGGGAATTTGTGTGTCATCGGACATGCTTCGCCCTACAGAACACA 489
QY 150 ValThrThrGlyIleValaSerThrAlaGlnArgGluGlyArgGluLeuArgAsp 169
Db 490 GTGACMAAGGACATCTGTCAGACATGCCAGGGGAGGAGGAGGAGCTGGCGGAGC 549
QY 170 SerAspMetAspTyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyPro 189
Db 550 TCCGACATGACATCATCAAGACGATCCATCATCACTACGGAACTCCGGGGAGACCA 609
QY 190 LeuValaLeuLeuAspGlyGluValaIleGlyIleAsnThrLeuLysValaThrAlaGlyIle 209
Db 610 CTGGTGAACCTGGAGATGGAGGTCAATTGGCATCAACAGCTCAAGTCAAGGCTGGCATC 669
QY 210 SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGln 229
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QY 220 IleLysAspTyrLysLysArgPheIleGlyIleArgMetArgThrIleTherProSerLeu 249
Db 730 ATCAAGAGCTGAGAGAGCGCTTCAATCCGACATACGAGTCCGACATCAACCAAGCTTG 789
QY 250 ValaAspGluLeuLysAlaSerAsnProAspPheProGluValaSerSerGlyIleTyVala 269
Db 790 GTGATAGAGTGAAGGACAGCAACCCGACCTTCCAGAGGTGACAGAGGAATTTATGTG 849
QY 270 GlnGluValaAlaProAsnSerProSerGlnArgGlyIleGlnAspGlyAspIleIle 289
Db 850 CAAGAGTGTGGCCGAATTCACCTTCTCAGAGAGGCGGACATCCAGAGGTGACATCTATC 909
QY 290 ValLysValaAsnGlyArgProLeuValaAspSerSerGluLeuGlnGluAlaValLeuThr 309
Db 910 GTCAAGGTCAACAGGCGTCTCTTACTGATCTGAGTGAAGCTGCAAGAGGCGGTGTCACC 969
QY 310 GluSerProLeuLeuGluValaArgArgGlyLysAsnAspAspLeuLeuPheSerIleAla 329
Db 970 GAGTCTCTCTCTTAAGTGAAGTGTGGGCGGAGGAGACGACCTCTTCAAGCATCCCA 1029

OY 330 ProgluValValMet 334
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 Db 1030 CCTGAGGTGTCATG 1044

RESULT 4 US-09-796-753-33

Sequence 33, Application US/09796753
 Publication No. US20030027998A1
 GENERAL INFORMATION:

APPLICANT: McCarthy, Sean A.

TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF

FILE REFERENCE: 7853-227-999

CURRENT APPLICATION NUMBER: US/09/796,753

CURRENT FILING DATE: 2001-03-01

PRIOR APPLICATION NUMBER: 09/183,175

PRIOR FILING DATE: 1998-10-30

PRIOR APPLICATION NUMBER: 09/223,094

PRIOR FILING DATE: 1998-12-30

PRIOR APPLICATION NUMBER: 09/223,546

PRIOR FILING DATE: 1998-12-30

PRIOR APPLICATION NUMBER: 09/224,246

PRIOR FILING DATE: 1998-12-30

PRIOR APPLICATION NUMBER: 09/259,388

PRIOR FILING DATE: 1999-02-26

PRIOR APPLICATION NUMBER: 60/122,458

PRIOR FILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: 09/312,359

PRIOR FILING DATE: 1999-05-14

PRIOR APPLICATION NUMBER: 09/336,536

PRIOR FILING DATE: 1999-06-18

PRIOR APPLICATION NUMBER: 09/342,687

PRIOR FILING DATE: 1999-06-29

PRIOR APPLICATION NUMBER: 09/345,464

PRIOR FILING DATE: 1999-06-30

PRIOR APPLICATION NUMBER: 09/365,164

PRIOR FILING DATE: 1999-07-30

PRIOR APPLICATION NUMBER: 09/399,723

PRIOR FILING DATE: 1999-09-20

PRIOR APPLICATION NUMBER: 09/409,634

PRIOR FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: 09/471,179

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: 09/474,071

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: 09/474,072

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: 09/514,010

PRIOR FILING DATE: 2000-02-25

PRIOR APPLICATION NUMBER: 09/516,745

PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: 09/572,002

PRIOR FILING DATE: 2000-05-14

PRIOR APPLICATION NUMBER: 09/597,993

PRIOR FILING DATE: 2000-06-19

PRIOR APPLICATION NUMBER: 09/599,596

PRIOR FILING DATE: 2000-06-22

PRIOR APPLICATION NUMBER: 09/630,334

PRIOR FILING DATE: 2000-07-31

PRIOR APPLICATION NUMBER: 09/606,565

PRIOR FILING DATE: 2000-06-29

PRIOR APPLICATION NUMBER: 09/606,317

PRIOR FILING DATE: 2000-06-29

PRIOR APPLICATION NUMBER: 09/665,666

PRIOR FILING DATE: 2000-09-20

PRIOR APPLICATION NUMBER: 09/677,751

PRIOR FILING DATE: 2000-09-30

NUMBER OF SEQ ID NOS: 162

SEQ ID NO 33

LENGTH: 1563

TYPE: DNA

ORGANISM: Mouse

US-09-796-753-33

Alignment Scores:

Pred. No.: 1,57e-175 Length: 1563
 Score: 1635.00 Matches: 325
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 97.4% Indels: 0
 DB: 3 Gaps: 0

US-10-617-443B-2 (1-334) x US-09-796-753-33 (1-1563)

OY 10 GLEUHIAGLLEUSETSERPROAGTYRYPHEANPHEILEAASPVALAIGLU 29
 |||||
 Db 337 GGCTCCACAGCTGAGCGCCGGCTCAAGTTCATCTCATCTGCTGAGTGGAG 396
 |||||
 OY 30 LYSILEAIPROAVALAHIILEGLUPELEUAIGHIAPROLEUPHEGLYARG 49
 |||||
 Db 397 AAGATCGACACCGCTGGTCCATAGAGCTCTTCCAGACACCCCGCTTTGGCCGC 456
 |||||
 OY 50 AENVALPROLEUSERSEGLYSEGLYPHEILEMETSERGLUALAGLYLEUILEIETHR 69
 |||||
 Db 457 AACGTGCCCTCTCCAGCGGTTCTGGCTTCATCATGTCAAGAGCCGCTGATCATACC 516
 |||||
 OY 70 AENALHISVALSERSEANSEALALAPROGLYARGINGLNULEUYAIGLN 89
 |||||
 Db 517 AATGCCACAGTGTGTCCAGCAACAGTCTGCCCGGACAGCAGCTCAAGGTGCAG 576
 |||||
 OY 90 LEUGIANGGLYASPSERTYGLUALATHRILEYSAAPILLEAPLYLSERTASPILE 109
 |||||
 Db 577 CTACAGAAATGGGACTCTTATGAGGCCACATCAAGACATCGACMAAGTCCGACATT 636
 |||||
 OY 110 ALATHRILEYLIEHISPROLYSELYSEUPROVALLEULEULEUGLYHISERALA 129
 |||||
 Db 637 GCCACCATCAGATCATCATCCAGAAAGAGCTCCCTGTTGTTGCTGGTCACTCGGCC 696
 |||||
 OY 130 AEPLEUATPROGLYGLUPHEVALAIALEIIEGLYSETPROPEALALEUGIABANTHR 149
 |||||
 Db 697 GACCTGCCGCTGGGAGATTGTGGTGCCATCGGACATCCCTTCGACCTACAGAACACA 756
 |||||
 OY 150 VALTHRIHNGLYILEVALISERTHRAAGLNIRGILUGIYARGGLUUEUGLYLEUARGASP 169
 |||||
 Db 757 GTGACAAAGGAGATGTGAGCACTGCCAGGAGGAGGAGGAGCTGGGCTCCGGGAGAC 816
 |||||
 OY 170 SERASPMECAAPTYRILEGLINTHRASPAIALEILEANTYRGLYAENSERGLYGLYPRO 189
 |||||
 Db 817 TCCGACATGAGCATCATCATCAGATGCCATCATCATCAGGGAATCCGGGGAGACCA 876
 |||||
 OY 190 LEUVALAENLEUASPGLYGLUVALILEGLYILEANTRILEUYSVALTHRALAGLYTLE 209
 |||||
 Db 877 CTGCTGAACCTGATGGAGGATGTCATTGGCATCAACGCTCAAGGTCAACGGCTGGCATC 936
 |||||
 OY 210 SERPHEALAIIEPROSERASPARGLIEHTRZRPHELEUTHRIUPHEGLNAPLYASGLIN 229
 |||||
 Db 937 TCCTTTGCCATTCCTTCAGACCGATCATCACAGGTTCTTCCAGAGAGTTCCAAAGACAGAG 996
 |||||
 OY 230 ILEYSAAPTPLYLYSARGPHEILEGLYILEARGMECATRTRILETHRPROSERLEU 249
 |||||
 Db 997 ATCAAAAGACTGGAAGAACGCTTCATGCGCATTAAGATGGGAGATCAACCAAGCTTG 1056
 |||||
 OY 250 VALASPGLULEULYVALASERASNPROASPHEPROGLUVALISERSERGLYILETYVAL 269
 |||||
 Db 1057 GTGGATGAGCTGAAGGCCAGCAACCCGACCTCCAGAGGCTCAACAGTGAATTATGTCG 1116
 |||||
 OY 270 GINGIUVAlAIPROANSEPRSESGIYNARGIYIGIYIIEGINAPSGIYASPIIIELE 289
 |||||
 Db 1117 CAAGAGTTGGCGGAATTCCTTCAGAGAGCGGACATCCAAAGATGGAGCATCATTC 1176
 |||||
 OY 290 VALYSAVALAENGILYARGPROLEUVALASPSERSEGLIUEUGINGIUALAVALLEUTHR 309
 |||||
 Db 1177 GTCAAGGTCAACGGGCGCTCTAGTGGACTCGAGTGAAGCGAGAGCGCTGCTGACC 1236
 |||||
 OY 310 GLUSERPROLEULEULEUGIUVAlARGARGIYANASAPPLEULEUPHESERTILEALA 329
 |||||

Db 1237 GAGTCTCCTCTCTAGAGAGTGGGGGGAAGAGACCTCTTTCAGATCCGA 1295
QY 330 ProgluValValMet 334
Db 1297 CCTGAGGTGGTCATG 1311

RESULT 5
US-10-275-505-28
Sequence 28, Application US/10275505
Publication No. US20040081961A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: DELEGANE, Angelo M.; LAL, Preeti G.
APPLICANT: HARPLIA, April J.A.; PATTERSON, Chandra
APPLICANT: WALIA, Natinder K.; KEARNEY, Liam
APPLICANT: TRIBOULEY, Catherine M.; KHAN, Farrah A.
APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.
APPLICANT: AZIMZAI, Valda; ELLIOTT, Vicki S.
APPLICANT: NGUYEN, Danielle B.; GANDHI, Ameena R.
APPLICANT: YANG, Junning; HERMANDEZ, Roberto
APPLICANT: POLICKI, Jennifer L.; LU, Dying Anna M.
APPLICANT: REDDY, Roopa M.; YUE, Henry
APPLICANT: TANG, Y. Tom
TITLE OF INVENTION: PROTEASES
FILE REFERENCE: PI-0085 USN
CURRENT APPLICATION NUMBER: US/10/275,505
PRIOR APPLICATION NUMBER: PCT/US01/14651
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/209,402
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: 60/207,477
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/205,803
PRIOR FILING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: 60/203,566
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 60/202,082
PRIOR FILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PERL Program
SEQ ID NO 28
LENGTH: 1797
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 7474343CB1
US-10-275-505-28

Alignment Scores:
Pred. No.: 1,92e-175 Length: 1797
Score: 1635.00 Matches: 325
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 97.4% Indels: 0
Gaps: 0
DB: 7

US-10-617-443b-2 (1-334) x US-10-275-505-28 (1-1797)

QY 10 GYLeuHISGLLeuSerSerProArgTyrTyrPheAsnPheIleAlaAspValValGlu 29
Db 565 GGTCTCCACCACTAGACGCGCGGCTACAGATTCACTTCACTGCTGACGTTGGGAG 624
QY 30 LysIleAlaProAlaValValHisIleGluLeuPheLeuArgHisProLeuPheGlyArg 49
Db 655 AAGATCGACCAACGCGTGTCTCCACATAGAGCTCTTCTGAGACACCCCGCTGTTGGCCGC 684
QY 50 AsnValProLeuSerSerGlySerGlyPheIleMetSerGluAlaGlyLeuIleThr 69
Db 685 AACGGGCCCCCTTCCAGCGGTTCTGCTTCATCATGTCTGAGAGCGCGGCTGATCATACC 744
QY 70 AsnAlaHisValValSerSerAsnSerAlaAlaProGlyArgGlnGlnLeuValGln 89

Db 745 AATGCCCACTGTGTCTCAGACACAGTCTCTCCCGGCAAGACAGCACTCAAGTTCAG 804
QY 90 LeuGlnAsnGlyAspSerTyrGluAlaThrIleLysAspIleAspLysSerAspIle 109
Db 805 CTACAGAAATGGGACTCTCTATGAGGCCACATCAAGACATGACMAAGTCGACATT 864
QY 110 AlaThrIleLysIleHisProLysLysLeuProValIleLeuLeuGlyHisSerAla 129
Db 865 GCCACCATCAAGATCATCCAGAGAAAGCTCCCTGTGTGTCTGTGATCTCGGCC 924
QY 130 AspLeuArgProGlyGluPheValValAlaIleGlySerProPheAlaLeuGlnAsnThr 149
Db 925 GACCTCGCGCTGGGAGATTGTGTGGCCATTCGCAATCCTTCGCCCTACAGAACACA 984
QY 150 ValThrThrGlyIleValSerThrAlaGlnArgGluGlyArgGluLeuArgAsp 169
Db 985 GTGACAAAGGCGCATGTGACACTGCCAGCGGGGAGGAGGAGCTGGGCTCCGGGAC 1044
QY 170 SerAspMetAspTyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyPro 189
Db 1045 TCCGACATGACTCATCATCAGAGATCCATCATCAACGAGGAACTCCGGGGAGACCA 1104
QY 190 LeuValAsnLeuAspGlyGluValIleGlyIleAsnThrLeuLysValThrAlaGlyIle 209
Db 1105 CTGCTGAACCTGAGATGGGAGGTCAATTGGATCAACAGCTCAAGTCAAGCTGGCATC 1164
QY 210 SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGln 229
Db 1165 TCCTTGGCATCCCTCAGACCGCATCAACGGTTCCTCAGAGATTCCAGAGATTCCAGAGCAG 1224
QY 230 IleLysAspTyrPheLysArgPheIleGlyIleArgMetArgThrIleThrProSerLeu 249
Db 1225 ATCAAAAGCTGAAGAAACGCTCTCATCGGCATACGGAAGCGGACATCAACAGCCG 1284
QY 250 ValAspGluLeuLysAlaSerAsnProAspPheProGluValSerSerGlyIleTyrVal 269
Db 1285 GTGATGATGCTGAAGCCAGACACCGGACTTCCAGAGGTGACGAGGAATTATGAG 1344
QY 270 GlnGluValAlaProAsnSerProSerGlnArgGlyIleGlnAspGlyAspIleIle 289
Db 1345 CAAGAGTTGGCGCCAAATTCACCTTCTCAGAGAGCGGACATCCAAAGTGTGACATCATC 1404
QY 290 ValLysValAsnGlyArgProLeuValAspSerSerGluLeuGlnAlaValLeuThr 309
Db 1405 GTCAAGGTCAACGGCGCTCTCTAGTGACTGAGTGAAGCTGCAAGAGCGCTGACCC 1464
QY 310 GluSerProLeuLeuGluValAlaArgArgLysAsnAspAspLeuLeuPheSerIleAla 329
Db 1465 GAGTCTCCTCTCTACTGAGGTGGCGGGGGAAGAGACACCTCTTCAAGCATCCGA 1524
QY 330 ProgluValValMet 334
Db 1525 CCTGAGGTGGTCATG 1539

RESULT 6
US-11-140-224-28
Sequence 28, Application US/11140224
Publication No. US20050227280A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: DELEGANE, Angelo M.; LAL, Preeti G.
APPLICANT: HARPLIA, April J.A.; PATTERSON, Chandra
APPLICANT: WALIA, Natinder K.; KEARNEY, Liam
APPLICANT: TRIBOULEY, Catherine M.; KHAN, Farrah A.
APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.
APPLICANT: AZIMZAI, Valda; ELLIOTT, Vicki S.
APPLICANT: NGUYEN, Danielle B.; GANDHI, Ameena R.
APPLICANT: YANG, Junning; HERMANDEZ, Roberto
APPLICANT: POLICKI, Jennifer L.; LU, Dying Anna M.
APPLICANT: REDDY, Roopa M.; YUE, Henry
APPLICANT: TANG, Y. Tom
TITLE OF INVENTION: PROTEASES


```

QY 50 AsnValProLeuSerSerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThr 69
Db 192 AACGTGCCCCCTGTCCAGAGCGTTCTGGCTTCATCATGTCAGAGGCCGGCTGATCATCAC 251
QY 70 AsnAlaHisValValSerSerAsnSerAlaAlaProGlyArgGlnGlnLeuValGln 89
Db 252 AATGCCCAAGTGTGTCCAGCAACAGTCTGCCCGGACAGGCAACAGCTCAAGGTGAG 311
QY 90 LeuGlnAsnGlyAspSerTyrGlnAlaThrIleIleAspIleLeuGlyLeuSerAspIle 109
Db 312 CTACGAATGGGGACTCTCTATAGAGCCACATCAAGACATGACAGAGAGTGGACAT 371
QY 110 AlaThrIleLeuValLeuIleProGlyValLeuProValLeuLeuLeuGlyHisSerAla 129
Db 372 GCCACCATCAAGATCATCTCCAGAAAGAGTCCCTGTGTCTTCTGCTGGTCACTCGGCC 431
QY 130 AspLeuArgProGlyGlnPheValAlaIleGlySerProPheAlaLeuGlnAsnThr 149
Db 432 GACCTGCGCGCTGGGGAGTTGTGTGGCCATCGGACATCCCTTCCCTACAGAACACA 491
QY 150 ValThrThrGlyIleValSerThrAlaGlnArgGlnGlyArgGlnLeuGlyLeuArgAsp 169
Db 492 GTGACAAAGCGCATCTGTACAGCATGCTCCAGCGGGAGGAGGAGCTGGCTCGGGAGC 551
QY 170 SerAspMetAspTyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyPro 189
Db 552 TCCGACATGACATCATCTCAAGCGATGCCATCATCACTACGGGAACTCCGGGGAGACA 611
QY 190 LeuValAsnLeuAspGlyGlnValIleGlyIleAsnThrLeuValThrAlaGlyIle 209
Db 612 CTGGGAACTCGATGCGAGGTGATGTGGCATCAACGCTCAAGGTCAAGCTCGGCTGGCATC 671
QY 210 SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGlnPheGlnAspIleGln 229
Db 672 TCTTTGGCATCTCCCTCAGACCGCATCAACGCTTCTCCACAGAGTCCCAAGACAAAGAG 731
QY 230 IleuAspTyrPheValLeuArgPheIleGlyIleArgMetArgThrIleThrProSerLeu 249
Db 732 ATCAAAAGCTGGAGAAAGCGCTTCATCGGCATACCGATCGGACATCAACCAAGCCTG 791
QY 250 ValAspGluLeuValLeuSerAsnProAspPheProGluValSerSerGlyIleTyrVal 269
Db 792 GTGATGAGCTGAGAGCGGAGCAACCGGACTTCCAGAGGTGACAGCATGGAATTTATGTG 851
QY 270 GlnGlnValAlaProAsnSerProSerGlnArgGlyIleGlnAspGlyAspIleIle 289
Db 852 CAAGAGGTGGCGCCAAATTCATCTTCAGAGAGCGGATCCAAAGATGGTGACATCATC 911
QY 290 ValLeuValAsnGlyArgProLeuValAspSerSerGluLeuGlnAlaValLeuThr 309
Db 912 GTCAAGGTCAACGGCGGCTCTTATGTGACTGAGTGAAGCTGCAAGAGGCCCTGCTGACC 971
QY 310 GluSerProLeuLeuLeuGlnValAlaArgArgIleAsnAspAspLeuLeuPheSerIleAla 329
Db 972 GAGTCTCTCTCTCTCTGAGAGGTGGGGGGGAGAAAGACATCTCTTTCAGCATCGCA 1031
QY 330 ProGluValValMet 334
Db 1032 CCTGAGGTGTCATG 1046

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RESULT 8

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US-10-381-820A-7
; Sequence 7, Application US/10381820A
; Publication No. US2004014233A1
; GENERAL INFORMATION:
; APPLICANT: Deshun, Lu
; APPLICANT: Song, Ho Yeong
; APPLICANT: Su, Eric Men
; APPLICANT: Wang, He
; TITLE OF INVENTION: Novel Secreted Proteins and Their Uses
; FILE REFERENCE: X-13974
; CURRENT APPLICATION NUMBER: US/10/381,820A
; CURRENT FILING DATE: 2003-03-27

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; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 2094
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (206)..(1564)
US-10-381-820A-7

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Alignment Scores:

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Pred. No.: 2,4e-175 Length: 2094
Score: 1635.00 Matches: 325
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: Gaps: 0

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US-10-617-443B-2 (1-334) x US-10-381-820A-7 (1-2094)

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QY 10 GlyLeuHisGlnLeuSerSerProArgTyrIlePheAsnPheIleAlaAspValValGln 29
Db 590 GGTCTCCACCAAGTCGAGGAGCGCCCGCTCAAGATTCACTTCATGTCGAGCGGCTGATCATCAC 649
QY 30 LysIleAlaProAlaValAlaHisIleGlnPheLeuArgHisProLeuPheGlyArg 49
Db 650 AAGATGACCAAGCGCGTGTCTCACTAGAGCTTCTTCCAGACACCCTGTTTGCCGCC 709
QY 50 AsnValProLeuSerSerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThr 69
Db 710 AACGTGCCCCCTGTCCAGAGCGTTCTGGCTTCATCATGTCAGAGGCCGGCTGATCATCAC 769
QY 70 AsnAlaHisValValSerSerAsnSerAlaAlaProGlyArgGlnGlnLeuValGln 89
Db 770 AATGCCCAAGTGTGTCCAGCAACAGTCTCCCGGACAGGACACTCAAGGTGAG 829
QY 90 LeuGlnAsnGlyAspSerTyrGlnAlaThrIleIleAspIleLeuGlyLeuSerAspIle 109
Db 830 CTACGAATGGGAGACTCTCTATAGAGCCACATCAAGACATGACAGAGAGTGGACATT 889
QY 110 AlaThrIleLeuValLeuIleProGlyValLeuProValLeuLeuLeuGlyHisSerAla 129
Db 890 GCCACCATCAAGATCATCTCCAGAAAGAGTCCCTGTGTCTGCTGGTCACTCGGCC 949
QY 130 AspLeuArgProGlyGlnPheValAlaIleGlySerProPheAlaLeuGlnAsnThr 149
Db 950 GACCTGCGCGCTGGGGAGTTGTGTGGCCATCGGACATCCCTTCCCTACAGAACACA 1009
QY 150 ValThrThrGlyIleValSerThrAlaGlnArgGlnGlyArgGlnLeuGlyLeuArgAsp 169
Db 1010 GTGACAAAGCGCATCTGTACAGCATGCTCCAGCGGGAGGAGGAGCTGGCTCGGGAGC 1069
QY 170 SerAspMetAspTyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyPro 189
Db 1070 TCCGACATGACATCATCTCAAGCGATGCCATCATCACTACGGGAACTCCGGGGAGACA 1129
QY 190 LeuValAsnLeuAspGlyGlnValIleGlyIleAsnThrLeuValThrAlaGlyIle 209
Db 1130 CTGGTGAACCTGATGCGGAGGTGATGTGGCATCAACAGCTCAAGGTCAAGCTGCGGATC 1189
QY 210 SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGlnPheGlnAspIleGln 229
Db 1190 TCTTTGGCATCTCCCTCAGACCGCATCAACGCTTCTCCACAGAGTCCCAAGAGACAGAG 1249
QY 230 IleuAspTyrPheValLeuArgPheIleGlyIleArgMetArgThrIleThrProSerLeu 249
Db 1250 ATCAAAAGCTGGAGAAAGCGCTTCATCGGCATACGGAGTGGGAGATCAACCAAGCCTG 1309
QY 250 ValAspGluLeuValLeuSerAsnProAspPheProGluValSerSerGlyIleTyrVal 269
Db 1310 GTGATGAGCTGAGAGCGGAGCAACCGGACTTCCAGAGGTGACAGCATGGAATTTATGTG 1369

```

```
QY 270 GINGLUVAlA1AProAmsenProSerGlnArgGlyYllEglnAaspGlyAapIlelle 289
| | | | |
DB 1370 CAGAGGTTGCCCGCAATTCACCTTCTCAGAGAGGGCGCATCCAGATGGTGCATCATC 1429
QY 290 VALLYSVALA1AProAmsenProSerGlnArgGlyYllEglnAaspGlyAapIlelle 309
| | | | |
DB 1430 GTCAGAGTCAACGGGCGTCTCTAGTGAAGTCAAGTGAAGGAGGCGGCTGAGCC 1489
QY 310 GUSERProLeuLeuGlnGluValArgArgGlyAAspAAspLeuLeuPheSerIlella 329
| | | | |
DB 1490 GAGTCTCTCTCTCTACTGAGGTGCGCGGGAGACGACGACTCTCTTCAGCATGCA 1549
QY 330 ProGluValValMet 334
| | | | |
DB 1550 CCTGAGGTGTCATG 1564

RESULT 9
US-10-956-157-5181
; Sequence 5181, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patent version 3.2
; SEQ ID NO 5181
; LENGTH: 2541
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-5181

Alignment Scores:
Pred. No.: 3,18e-175 Length: 2541
Score: 1635.00 Matches: 325
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 97.4% Indels: 0
Gaps: 0
DB: 9

US-10-617-443B-2 (1-334) x US-10-956-157-5181 (1-2541)
QY 10 GLYLEuHIGlnLeuSerSerProAArgTTLyPheAAspPheIlellaAAspValValGlu 29
| | | | |
DB 589 GGTCTCCACCAAGTTCAGAGCCCGCGCTCAAGTTCAACTTCATGCTGACGTGTGAG 648
QY 30 LysIleAlAProAlaValValHisIleGluLeuPheLeuArgHisProLeuPheGlyArg 49
| | | | |
DB 649 AAGATGCCACCAAGCGGTGTCCATAGAGCTTCTCTAGAGACCCCGCTTTGGCCCG 708
QY 50 AAspValProLeuSerSerGlySerGlyPheIleMetSerGlnAagIlyLeuIleIleThr 69
| | | | |
DB 709 AACGTCCCGCTGTCAGAGCGGTCTGAGCTTCATGATGACAGGCGCGCTGATCATCAC 768
QY 70 AAspAlaHisValValSerSerAAspSerAlaAlaProGlyArgGlnGlnLeuValGln 89
| | | | |
DB 769 AATGCCACCGAGTGTCTCAGCAACAGTGTGCTCCCGGCGAGGAGGAGCTCAAGGTGAG 828
QY 90 LeuGlnAAspGlyAAspSerTyrGluAlaThrIleLysAAspIleAAspLysLysSerAAspIle 109
| | | | |
DB 829 CTAACAGAAATGGGACCTCTATGAGGCCACATCAAAAGACATGACAGAAAGTGTGACATT 888
QY 110 AlaThrIleLysIleHisProLysLysLeuProValLeuLeuLeuGlyHisSerAla 129
| | | | |
DB 889 GCCACCATCAAGATCATCCCAAGAAAGCTCCCTGTGTGTGTGTGCTGGGTCACTGGGCC 948
QY 130 AAspLeuArgProGlyGluPheValValAlaIleGlySerProPheAlaLeuGlnAAspThr 149
| | | | |
DB 949 GACCTGCGGCTGGGAGTTTGTGTGGCCATCGGACGTCCCTTCGCCCTCAAGAACACA 1008
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QY 150 ValThrThrGlyIleValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAAsp 169
| | | | |
DB 1009 GTGACACCGGCGATGTCATGACACTGCCAGCGGGAGGGCAGGAGCTGGGCTCCGGGAC 1068
QY 170 SerAAspMetAAspTyrIleGlnThrAAspAlaIleIleAAspTyrGlyAAspSerGlyPro 189
| | | | |
DB 1069 TCCGACATGAGACTCATCATCAAGCGGATCCATCACTACCGGGAATCCCGGGGAGACCA 1128
QY 190 LeuValAAspLeuAAspGlyGluValIleGlyIleAAspThrLeuValThrAlaGlyIle 209
| | | | |
DB 1129 CTGTGAACCTGGAGTGGAGGTCTCATGACATCAACAGCTCAAGTCAAGCTGACATC 1188
QY 210 SerPheAlaIleProSerAAspArgIleThrArgPheLeuThrGluPheGlnAAspLysGln 229
| | | | |
DB 1189 TCTTTGGCATTCCTTCAGACCGCATCACAGGTTCTTCACAGAGTTCCAGACAGACAG 1248
QY 230 IleLysAAspTyrPylsLysArgPheIleGlyIleArgMetArgThrIleThrProSerLeu 249
| | | | |
DB 1249 ATCAAAAGACTGGAAAGAGCGCTTCATCGGCATACAGATGCGGACGATCACACCAAGCCTG 1308
QY 250 ValAAspGluLeuLysAlaSerAAspProAAspPheProGluValSerSerGlyIleTyrVal 269
| | | | |
DB 1309 GTGATGAGCTGAAGGCCAGCAACCGGACTTCCAGAGGTCAAGCATGTAATTTATGTG 1368
QY 270 GINGLUVAlA1AProAmsenProSerGlnArgGlyYllEglnAaspGlyAapIlelle 289
| | | | |
DB 1369 CAGAGGTTGGCGCGCAATTCACCTTCTCAGAGAGGCGGCATCCAGAGGTGATCATCATC 1428
QY 290 VALLYSVALA1AProAmsenProLeuValAAspSerSerGluLeuGlnGluValValLeuThr 309
| | | | |
DB 1429 GTCAGAGTCAACGGGCGTCTCTACTGAGCTCGAGTGAAGTGCAGAGAGCGGTGTGACC 1488
QY 310 GUSERProLeuLeuGlnGluValArgArgGlyAAspAAspLeuLeuPheSerIlella 329
| | | | |
DB 1489 GAGTCTCTCTCTCTAGAGGTGCGCGGGAGACGACGACTCTCTTCAGCATTCGCA 1548
QY 330 ProGluValValMet 334
| | | | |
DB 1549 CCTGAGGTGTCATG 1563

RESULT 10
US-10-485-313A-31
; Sequence 31, Application US/10485113A
; Publication No. US20050059002A1
; GENERAL INFORMATION:
; APPLICANT: NTE, Guilting
; APPLICANT: SALAMONSEN, Lois Adrienne
; APPLICANT: Li, Ying
; APPLICANT: HAMPTON, Anne Lorraine
; APPLICANT: FINDLAY, John Kerr
; TITLE OF INVENTION: Novel Serine Protease
; FILE REFERENCE: 31633-200357
; CURRENT APPLICATION NUMBER: US/10/485,313A
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: PCT/AU02/01010
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: PR6707
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patent version 3.1
; SEQ ID NO 31
; LENGTH: 2543
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-485-313A-31

Alignment Scores:
Pred. No.: 3,18e-175 Length: 2543
Score: 1635.00 Matches: 325
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 97.4% Indels: 0
```


DB: 9 Gaps: 0
US-10-617-443b-2 (1-334) x US-10-485-313A-31 (1-2543)
QY 10 GLEUHSGLNLSerSerProArgTyrLysPheAsnPhelAlaAspValValGlu 29
Db 577 GGTCTCCACGAGCTGAGCAGCCCGGCTACAGATTCACTTCATGTCGACGTGTGGAG 636
QY 30 LysIleAlaProAlaValValHisIleGluLeuPheLeuArgHisProLeuPheGlyArg 49
Db 637 AAGATCGACCAAGCCGCTGCTCCATAGAGCTCTTCCGAGACACCCGCTGTGGCCGC 696
QY 50 AsnValProLeuSerSerSergLysPheIleMetSergLysAlaGlyLeuIleIleThr 69
Db 697 AACGGCCCTCTCCAGCGGTTCTGCTTCATCATCTCAGAGCCGGCTGATCTACCC 756
QY 70 AsnAlaHisValValSerSerAsnSerAlaAlaProGlyArgGlnLeuLysValGln 89
Db 757 AATGCCACGTGTGTCCAGCAACAGTGTGCTCCCGGAGGACAGCTCAAGGTGCAG 816
QY 90 LeuGlnAsnGlyAspSerTyrGlnAlaThrIleLysAspIleAspLysSerAspIle 109
Db 817 CTACGAATGGGAGCTCTATGAGGCCACCATCAAGACATCGACAAAGATCGACATT 876
QY 110 AlaThrIleLysIleHisProLysLysLeuProValLeuLeuGlnYHisSerAla 129
Db 877 GCCACCATCAAGATCTCATCCCAAGAAAAGCTCCCTGTCTTGTCTGGGTCACTCGCC 936
QY 130 AspLeuArgProGlyGluPheValValAlaIleGlySerProPheAlaLeuGlnAsnThr 149
Db 937 GACCTCGGCGCTGGGAGATTGTGTGGTCATCGGACAGTCCCTCGCCCTACAGAACCA 996
QY 150 ValThrThrGlyIleValSerThrAlaGlnArgGluGlyArgGlnLeuGlyLeuArgAsp 169
Db 997 GTGAAACGGGATGTGACGACCTGCCAGCGAGGCGAGGAGACTGGGCTCTCGGAGAC 1056
QY 170 SerAspMetAspTyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyPro 189
Db 1057 TCCGACATGAGTACATCCAGACGATGCCATCATCACTACGGGAATCCCGGGAGACA 1116
QY 190 LeuValAsnLeuAspGlyGluValIleGlyIleAsnThrLeuLysValThrAlaGlyIle 209
Db 1117 CTGGGAACCTGGAATGGCGAGGTGATGGCATCAACAGCTCAAGGTCAAGGCTGGCATC 1176
QY 210 SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGlnPheGlnAspIleGln 229
Db 1177 TCTCTTGGCATCCCTCAGACCGCATCAACGAGTCTCCACAGAGTCCMAAGACAGCAG 1236
QY 230 IleLysAspTyrLysArgPheIleGlyIleArgMetArgThrIleThrProSerLeu 249
Db 1237 ATCAAGACCTGGAGAGAGGCGCTTCATCGGCATACGGAATGCCAGCATCACACCAAGCCTG 1296
QY 250 ValAspGluLeuLysAlaSerAsnProAspPheProGluValSerSergLysIleTyrVal 269
Db 1297 GTGATGAGCTGAAAGCCAGCAACCCGAGCTCCCAAGGTGAGCAGTGAATTTATGAG 1356
QY 270 GlnGluValAlaProAsnSerProSergLysGlyIleGlnAspGlyAspIleIle 289
Db 1357 CAAGAGGTGGCCCAATTCATCTTCTCAGAGAGCGGATCCAAAGATGTGTACATCATC 1416
QY 290 ValLysValAsnGlyArgProLeuValAspSerSergLysLeuGlnGlnAlaValLeuThr 309
Db 1417 GTCAAGGTCAACGGGCGTCTTATGACTGAGTGAAGCTCAGAGAGCCGCTGAGACC 1476
QY 310 GlnSerProLeuLeuGlnValAlaArgArgGlyAsnAspAspLeuPheSerIleAla 329
Db 1477 GAGTCTCTCTCTCTACTGAGAGGTGCGGCGGGAACAGACCTCTCTTACGATCGCA 1536
QY 330 ProGluValValMet 334
Db 1537 CCGAGGTGTCTATG 1551
RESULT 11

US-09-796-753-31
Sequence 31, Application US/09796753
Publication No. US20030027998A1
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-227-999
CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 09/223,094
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/224,246
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/259,388
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/122,458
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 09/312,359
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/336,536
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 09/342,687
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 09/345,464
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/365,164
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 09/399,723
PRIOR FILING DATE: 1999-09-20
PRIOR APPLICATION NUMBER: 09/409,634
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 09/471,179
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 09/474,071
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/474,072
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/514,010
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: 09/516,745
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/572,002
PRIOR FILING DATE: 2000-05-14
PRIOR APPLICATION NUMBER: 09/597,993
PRIOR FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 09/599,596
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/630,334
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 09/606,565
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/606,317
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/665,666
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 09/677,751
PRIOR FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 31
LENGTH: 2576
TYPE: DNA
ORGANISM: Homo sapiens
US-09-796-753-31
Alignment Scores:
Pred. No.: 3,24e-175 Length: 2576
Score: 1635.00 Matches: 325
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0

Query Match: 97.4% Indels: 0
DB: 3 Gaps: 0
US-10-617-443b-2 (1-334) x US-09-796-753-31 (1-2576)

QY 10 G1YLeuH1eN1eSseRSeRProArGTYrLYsPheAnPhe11eAlAAsPValValGlu 29
DB 606 GGCTTCACAGCTGAGCCGCGGCTTCAGAGTTCACTTCATGTCGAGCTGGTGGAG 665
QY 30 Lys11eAlAProAlaVal1H1e1eG1uLeuPheLeuA9H1eProLeuPheG1YArg 49
DB 666 AAGATGCGACAGCGCGTGGTCCATAGAGCTTCTCTAGAGACCGCGCTGTTGGCGGC 725
QY 50 AAsnValProLeuSeSeSeRSeRg1YSeRg1YpHe11eMeSeRg1uAlG1YLeu11e1eTh 69
DB 726 AACGTCCCCCTGTCAGCGGTTCTGCTTCATCATATGTCAGAGGCCGCGCTGATCATACC 785
QY 70 AAsnAlH1eVal1ASeSeASeSeRAlAAlAProG1YArgG1uN1eLeu1YValG1u 89
DB 786 AATGCCACCTGCTGTCAGCAACAGTGGTCCCGGCGAGGAGCAGCTCAAGGTGCAG 845
QY 90 LeuG1uAAsnG1YAsPSeRg1YVal1A1eThr11eLYsAPR11eAsP1Ys1eSeRAsP1e 109
DB 846 CTACAGATGGGAGCTCTATGAGGCCATCAAGACATGCAAGAAAGATCGACAT 905
QY 110 AlAThr11eLYs11eH1sPProLYsLYsLeuProVal1LeuLeuG1YH1sSeRAlA 129
DB 906 GCCACCATCAAGATCCATCCCAAGAAAGAGCTCCCTGTTGTTGCTGGTGCATCGGCC 965
QY 130 AsPLeuArPProG1Yg1uPheVal1Al1eG1YSeRProPheAlA1eG1uN1eA1eTh 149
DB 966 GACCTGGCGCTGGGAGTTGTGTGGTCCATCGGCGCTCCCTGCGCTTACAGAAACAC 1025
QY 150 ValThrThrG1Y11eVal1SeRThrAlA1eArG1uG1YArgG1uLeuG1YLeuArAsP 169
DB 1026 GTGCAACGGGCACTGTCAGACATGCCACGGAGGGAGGAGCTGGGCTCCGGGAC 1085
QY 170 SeRAsPMeArP1Yr11eG1nThrAsPAl1e11eAAsnTYrG1YAsnSeRg1Yg1YPro 189
DB 1086 TCCGACATGAGCTACATCCAGACGAGTCCATCACTAACGGAACTCCGGGGAGCCA 1145
QY 190 LeuVal1AsnLeuAsP1Yg1YVal11eG1Y11eAAsnThrLeuLYsVal1ThrAlA1eG1Y 209
DB 1146 CTGGTGAACCTGAGTGGGAGGATGAGTGCATCAACGCTCAAGGTCAACGCGTGGCATC 1205
QY 210 SeRPhaAl1ePProSeRAsPArG11eThrArPHeLeuThrG1uPheG1uAAsP1Yg1u 229
DB 1206 TCTCTTGGCATCCCTCGACGAGCATCACGCTTCTCAAGAGTTCCAAAGACAGCAG 1265
QY 230 11eLYsArP1YrLYsLYsArPHe11eG1Y11eArGMeTArGThr11eThrProSeR1eU 249
DB 1266 ATCAAAAGACTGGAAGAACGCTTCATCGGCATACGAGTGGAGGATCACCAAGCCTG 1325
QY 250 Val1eP1YLeuLYsAlASeRAsnPProAsPHePProG1uVal1SeSeRg1Y11eTYrVal 269
DB 1326 GTGGATGAGCTGAGGCGGAGCCAGCACTTCCAGAGGTCAAGAGTGAATTATATGTG 1385
QY 270 G1uN1eVal1A1AProAsnSeRProSeRg1nArG1Yg1Y11eG1nAsP1YAsP11e11e 289
DB 1386 CAAGAGGTGGCGCAATTCACCTTCTCAGAGAGCGGCAATCAAGATGGTGAATCTATC 1445
QY 290 ValLYsVal1AAsnG1YArGProLeuVal1AsPSeSeRg1uLeuG1uN1eVal1e1eTh 309
DB 1446 GTCAAGGTCAACGGGAGTCTCTTATGACATCGATGAGCTGCAGAGAGCGGTGTCAGC 1505
QY 310 G1uSeRProLeuLeuG1uVal1ArgArG1YAsnAsPAsPLeuLeuPheSeR11eAlA 329
DB 1506 GAGTCTCTCTCTCTATGAGAGGTGCGGCGGGAACGAGACCTCTCTTCAAGCATCGCA 1565
QY 330 ProG1uVal1ValMet 334
DB 1566 CCTGAGGTGATCATG 1580

RESULT 12
US-10-485-313A-26
; Sequence 26, Application US/10485313A
; Publication No. US20050059002A1
; GENERAL INFORMATION:
; APPLICANT: NIF, Guiying
; APPLICANT: SALAMONSEN, Lois Adrienne
; APPLICANT: LI, Ying
; APPLICANT: HAMPTON, Anne Lorraine
; APPLICANT: FINDLAY, John Kerr
; TITLE OF INVENTION: Novel Serine Protease
; FILE REFERENCE: 31633-200357
; CURRENT APPLICATION NUMBER: US/10/485,313A
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: PCT/AU02/01010
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: PR6707
; NUMBER OF SEQ. ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 2450
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-485-313A-26
Alignment Scores:
Pred. No.: 5 75e-164 Length: 2450
Score: 1536.00 Matches: 302
Percent Similarity: 96.6% Conservative: 13
Best Local Similarity: 92.6% Mismatches: 0
Query Match: 91.5% Indels: 0
DB: 9 Gaps: 0
US-10-617-443b-2 (1-334) x US-10-485-313A-26 (1-2450)

QY 9 AlAG1YLeuH1eN1eSseRSeRProArGTYrLYsPheAnPhe11eAlAAsPValVal 28
DB 526 TCTGGTCTCCACACAGCTGACCAAGTCCGCGGTACAAAGTTCACTTCATGCGGATGGTG 585
QY 29 G1uLYs11eAlAProAlaVal1H1e1eG1uLeuPheLeuA9H1eProLeuPheG1Y 48
DB 586 GAGAAAGTGGCGGAGCTGTGTGTCATAGAGCTTTCGAGACACCCCTGTTGGC 645
QY 49 ArgAsnValProLeuSeSeSeRg1YSeRg1YpHe11eMeSeRg1uAlG1YLeu11e1e 68
DB 646 CGGAATGTCCGCTGTCAGTGGCTCGGCTTCATCATGTCAAGACCGGTTGATCGTC 705
QY 69 ThrAsnAlH1eVal1ASeSeRAsnSeRAlAAlAProG1YArgG1uN1eLeu1YVal 88
DB 706 ACCAAGCCCAAGTGTGCTTCAGCTCCAGCACTGCTCCGCGGCGACAGCTGAAGGTG 765
QY 89 G1uLeuG1uAAsnG1YAsPSeRg1YVal1A1eThr11eLYsAPR11eAsP1Ys1eSeRAsP 108
DB 766 CAGCTGCAAGATGGGATGCTATGAGGCCACATCCAGGAGATGACAAAGATCGGAC 825
QY 109 11eAlAThr11eLYs11eH1sPProLYsLYsLeuProVal1LeuLeuG1YH1sSeR 128
DB 826 ATGGCAGATTTGATATCAACCCCAAGAAAGAGCTTCGTGTGCTGCTGGTCACTCA 885
QY 129 AlAAsPLeuArPProG1Yg1uPheVal1AlA1eG1YSeRProPheAlA1eG1uN1eA1eTh 148
DB 886 GCAAGACTGGGCTGGGAGATTCGATGGTGGCATGGGAGCCCTTGGCCGCAAGAC 945
QY 149 ThrValThrThrG1Y11eVal1SeRThrAlA1eArG1uG1YArgG1uLeuG1YLeuArG 168
DB 946 ACCGTGCAACGGGCAATTCAGACACTGCCACAGGAGTGGCAAGAGCTGGGTCTCCGG 1005
QY 169 AsPSeRAsPMeArP1Yr11eG1nThrAsPAl1e11eAAsnTYrG1YAsnSeRg1Yg1Y 188
DB 1006 GACTCAGACATGAGCTATATCCAGACCGAGTGCATCATCAATTCAGGAACCTCAGAGAGA 1065
QY 189 ProLeuVal1AsnLeuAsP1Yg1YVal11eG1Y11eAAsnThrLeuLYsVal1ThrAlA1eG1Y 208

Db 1066 CCCCTGGAGACCTGGATGGAGGTCTATCGGCATCAACAGCTCAAGGTTCAGCTGGC 1125
Qy 209 TLeSerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspLys 228
Db 1126 ATTCCTCTTGGCATCCCTCGATGTCATCAACGCTTCTCTCGAGTTCCAAAACAG 1185
Qy 229 GlnIleLysAspTrpLysLysArgPheIleGlyIleArgMetArgThrIleThrProSer 248
Db 1186 CATGTGAAGACCTGGAGAACGCTTCAATTGTCATCCGATCGGATCGGACATCAACGCAAGT 1245
Qy 249 LeuValAspGluLeuLysAlaSerAsnProAspPheProGluValSerSerGlyIleThr 268
Db 1246 TTGGTGAGAGAACTGAAGAGCGCCCAACCCAGCTTTCAGCGGTCAGCAGAGGAAATATAT 1305
Qy 269 ValGlnGluValAlaProAsnSerProSerGlnArgGlyIleGlnAspGlyAspIle 288
Db 1306 GTTCAGAGGTGGTCCCAATTCACCTTCTCAGAGAGGAGCATCCAAAGATGGCCACATC 1365
Qy 289 IleValLysValAsnGlyArgProLeuValAspSerSerGluLeuGlnAlaValLeu 308
Db 1366 ATGCTCAAGTCAATGGCCGCCCTGGCGGATTCACAGCTGACAGAGGCAAGTCTTG 1425
Qy 309 ThrGluSerProLeuLeuGluValArgArgGlyAsnAspAspLeuLeuPheSerIle 328
Db 1426 AACGAGTCTTCACTCTCTGAGGTGGCGGAGCATGATGATCTCTTCAAGCATC 1485
Qy 329 AlaProGluValAlaMet 334
Db 1486 ATCCCTGAGTGTGCATG 1503

RESULT 13

US-10-301-822-78
Sequence 78, Application US/10301822
Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatekar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: BURGART, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF COLON CANCER
FILE REFERENCE: MPM01-023P2RNM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 78
LENGTH: 2551
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (222) ... (1580)
US-10-301-822-78

Alignment Scores:

Pred. No.: 7.6e-158 Length: 2551
Score: 1482.50 Matches: 319
Percent Similarity: 97.64 Conservative: 0
Best Local Similarity: 97.64 Mismatches: 6
Query Match: 88.34 Indels: 7

DB: 6 Gaps: 0

US-10-617-443B-2 (1-334) x US-10-301-822-78 (1-2551)
Qy 10 GlyLeuHisGlnLeuSerSerProArgTrpLysPheAsnPheIleAlaAspValValGlu 29
Db 606 GGTCTCCACCACTGAGCAGCCCGGCTCAAGATTCACTTCATTCGAGCGTGTGAG 665
Qy 30 LysIleAlaProAlaValAlaHisIleGlnLeuPheLeuAspGlnAspProLeuPheGlyArg 49
Db 666 AAGATCGCACCAAGCGGTGTCACTAATGAGCTTCTTCGAGACACCCGCTGTGGCCG 725
Qy 50 AsnValProLeuSerSerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThr 69
Db 726 AACGTGCCCCCTGTCCAGGGGTTCGTTCATCATGTCAAGAGCGCGCTATATCAAC 785
Qy 70 AsnAlaHisValAlaSerSerAsnSerAlaAlaProGlyArgGlnGlnLeuLysValGln 89
Db 786 AATGCCCACTGTGTGTCCAGCAAGTGTCTCCCGGCGCAGCAGCCTCAAGGTGAG 845
Qy 90 LeuGlnAsnGlyAspSerTrpGluAlaThrIleLysAspIleAspLysSerAspIle 109
Db 846 CTACAGAAATGGGACTCTTATGAGGCCACATCAAGACATCGACAAAGCTGGACAT 905
Qy 110 AlaThrIleLysIleHisProLysLysLeuProValLeuLeuGlyIleIleSerAla 129
Db 906 GCCACATCAAGATTCATCCCAAGAAAAGCTCCCTGTGTGTCTGTGGTCACTGGCC 965
Qy 130 AspleuArgProGlyGluPheValAlaIleGlySerProPheAlaLeuGlnAsnThr 149
Db 966 GACCTGGCGGT- GGGAGATTGTGTGGTCATCGAGAT- CCTTCGCCCTACAGAACACA 1023
Qy 150 ValThrThrGlyIleValSerThrAlaGlnArgGluArgGlyLeuArgAsp 169
Db 1024 GTGACAAAC- GGCATCGT- AGCAGTGGCCAGG- GAGGCGAGAGAGTGGCTCGGAGAC 1080
Qy 170 SerAspMetAspTrpLysLeuGlnThrAspAlaIleIle-AsnTrpGlyAsnSerGlyLys 189
Db 1081 TCCGATGATGACTATCATACAGAGGATGCCATCATCAACCGGAACTCCGGGGAGC 1140
Qy 189 LysLeuValAsnLeuAspGlyGluValIleGlyIleAsnThrLeuLysValThrAlaGlyI 209
Db 1141 CACTGTGAACCTGGATGGCAGGTCAATTGGCATCAACACGCTCAAGGTCAAGCTGGCA 1200
Qy 209 LysSerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspLys 229
Db 1201 TCTCCTTGGCATCCCTCGACAGCGCATCACAGGTTCTCACAGAGTTCCAAAGCAAGC 1260
Qy 229 LysIleLysAspTrpLysLysArgPheIleGlyIleArgMetArgThrIleThrProSer 249
Db 1261 AGATCAAGACCTGTGAAGAGCGCTTCAATCGGATACGATCGGACGATCACACCAAGC 1320
Qy 249 euValAspGluLeuLysAlaSerAsnProAspPheProGluValSerSerGlyIleThr 269
Db 1321 TTGGTGAGTGAAGTGAAGCCAGCAACCGGACTTCCAGAGTCAAGCTGAATATTATG 1380
Qy 269 aGlnGluValAlaProAsnSerProSerGlnArgGlyIleGlnAspGlyAspIleI 289
Db 1381 TGCAAGAGTGGCCCGCAATTCCTCTCAGAGAGGCGGATCCAAATGATGTGACATCA 1440
Qy 289 LeuValLysValAsnGlyArgProLeuValAspSerSerGluLeuGlnAlaValLeu 309
Db 1441 TGTCTAAGTCAAGCGGCGTCTCTTAATGACTGAGTGAAGTCAAGAGCGCGTGTGAG 1500
Qy 309 hrGluSerProLeuLeuGluValArgArgGlyAsnAspAspLeuLeuPheSerIle 329
Db 1501 CCGAGTCTCTCTCTACTGAGAGTGGCGCGGAGGAACGACGACCTCTCTTCAAGCATCG 1560
Qy 329 AlaProGluValAlaMet 334
Db 1561 CACCTGAGTGTGCATG 1577

RESULT 14

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US-09-764-898-112
; Sequence 112, Application US/09764898
; Patent No. US2002090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0501
; CURRENT APPLICATION NUMBER: US/09/764,898
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION DATA REMOVED - consult PAMM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 112
; LENGTH: 1868
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-898-112

Alignment Scores:
Pred. No.: 3,91e-146 Length: 1868
Score: 1378.00 Matches: 275
Percent Similarity: 98.6% Conservative: 0
Best Local Similarity: 98.6% Mismatches: 4
Query Match: 82.1% Indels: 0
DB: 3 Gaps: 0

US-10-617-443b-2 (1-334) x US-09-764-898-112 (1-1868)

QY 56 GYSGEGLYPHEIETSERGIUAGLYLEUIGLEIETHRANALHISVALISER 75
DB 23 GGTTCGGCTTCATCATGTAGAGCCGGCTCATCTACCAATCCCAACGGTGTCC 82
QY 76 SERASER1AALAPROGIYARGINGLNULEU1YVALIGLNULEUINANGIYAPSER 95
DB 83 AGCAACAGCTCTGACCCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 142
QY 96 TYRGLUALATHRI1ELYVAPRI1EAPPLYVLSERAPRI1EALATHRI1ELYVLEIS 115
DB 143 TATGAGGCCACACATCAAGACATCGACAAAGATGCGACATGCAATCAAGATCAT 202
QY 116 PROLYS1YLSVLEUPROVALLEULEU1YHISER1AAPLEUATPROGIYGLU 135
DB 203 CCCAAGAAAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 262
QY 136 PHEVALVAL1A1LEGIYSERPROBHE1ALEUGINANTHRVAL1THRTG1Y1LE1 155
DB 263 TTGTGTGGTCATCGGACATGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 322
QY 156 SERTHRALAGINARGG1UGLYARG1ULEUG1YLEUARGAPSERAPMETASPTYR1 175
DB 323 AGCATCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 382
QY 176 G1ANTHRAPAL1A1LEI1EANTYR1GLYASNSER1YGLYPROLEUVAL1ASHLEU 195
DB 383 CAGAGGATGCGATCATCACTACGGGAACTCCGGGGAGCACTGAGAACTGGATG 442
QY 196 GLUVAL1LEGI1Y1LEANTHR1LEU1YVAL1THRALAG1Y1LESERPEHA1 215
DB 443 GAGGTCATGTCATCAACAGCTCAAGGTCACGGCTGACATCTCTTGGCATCCCT 502
QY 216 ASPARGL1ETRRARGPHELEUTHRG1UNHEGINAPLYSGIN1ELYASPT1PL 235
DB 503 GACCGCATCAACAGGTTCTCAAGAGTTCCAAAGCAAGATCAAGATCAAGAG 562
QY 236 ARGPH1LEGI1Y1LEARGMETARGTHRI1ETHRPROSERLEUVAL1ASGL1 255
DB 563 CGCTTCATCGGATCGGATCGGAGCATCAACCAACCTGAGATGAGCTGAGGCC 622
QY 256 SERANP1COAPHPH1PROG1UVAL1SERSEGI1Y1ETRYVAL1G1NG1UVAL1 275
DB 623 AGCAACCCGAGCTTCCCAAGGTCAAGCACTGGAATTTATGTGCAGAGAGTTGCC 682
QY 276 SERPROSEGINARG1YGL1Y1LEGLINAPGIYAPRI1E1VAL1YVAL1ASND 295
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DB 683 TCACTTCTCAGAGAGCGGATCCAAAGATGAGCATCATCTCAAGGTCAACGGGCG 742
QY 296 PROLEUVAL1ASPERSEGIU1EUGING1UVAL1LEU1THRG1USERPROLEU 315
DB 743 CCTTACTGAGCTCGAAGTGAAGTGCAGAGGCGGTCTGACCAAGTCTCTCTACT 802
QY 316 GLUVAL1ARGRG1YANASAP1LEU1PHESERI1EAL1APROGIUVAL1MET 334
DB 803 GAGGTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 859

RESULT 15
US-09-969-384-7
; Sequence 7, Application US/09969384
; Publication No. US20020192749A1
; GENERAL INFORMATION:
; APPLICANT: Moore, et al.
; TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: P0555P1
; CURRENT APPLICATION NUMBER: US/09/969,384
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10542
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/236,384
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/194,118
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-969-384-7

Alignment Scores:
Pred. No.: 5.02e-117 Length: 1695
Score: 1122.00 Matches: 243
Percent Similarity: 80.3% Conservative: 13
Best Local Similarity: 76.2% Mismatches: 33
Query Match: 66.8% Indels: 30
DB: 3 Gaps: 6

US-10-617-443b-2 (1-334) x US-09-969-384-7 (1-1695)

QY 10 G1YLEU1HISGL1LEUSERSE1PROARG1YR1YSPHEANPHE1A1ASPV1ALG 29
DB 229 GGTTCACACAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 288
QY 30 LVY1EAL1PROAL1VAL1H1B1LEGI1LEU1PHELEUARGH1A1PROLEUPHE 49
DB 289 AAGATGACACAGCCCTGTGTCACATAGAGCTCTTCTGAGACACCCGCTGTT 348
QY 50 AENVAL1PROLEUSERSEGIYSEGIYPHEI1E1E1E1E1E1E1E1E1E1E1 69
DB 349 AACGTCCCTGTCAGCGGCTTCTGCTTCATCATGTGAGAGCGCGCTGATCAT 408
QY 70 ASMALHISVAL1A1SERSE1ASNSER1AAL1APROGIYARGING1NULEU1 89
DB 409 AATGCCACAGTGTGTCCAGCAACAGTGTGCCCCCGGAGGAGGAGGAGGAGG 468
QY 90 LEUG1ANAG1YAPSER1YR1Y1A1ATHRI1ELYVAPRI1EAPPLYVLSERAP 109
DB 469 CTACAGAAATGGGAGCTCTTAGGCGCACCATCAAGACATGACAAAGTCGACAT 528
QY 110 ALATHRI1ELY1LEH1SPROLY1YLYLEU1PROVAL1LEU1EUG1YHISER 129
DB 529 GCCACATCAAGATCATCCCAAGAAAGCTCCGTGTGTGTGCTGGGCTCACTG 568
QY 130 ASPLEUARGPROGIYGLUPHEVAL1A1A1LEGI1SERPROBHE1ALEUGIN 149
DB 589 GACCTGGGCTGGGAGGAGTTGTGTGGCCATGAGGAGTCTTCCCTTCCCTCA 648
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Qy 150 ValThrThrGlyIleValSerThrAlaGlnArgGluGlyLeuGlyLeuArgAsp 169
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    |||||
Qy 170 SerAspMetAspTyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyPro 189
    |||||
Db 709 TCCGACATGACATCACTACAGCGGATCGCATCACTACGGGAATCCGGGGGACCA 768
    |||||
Qy 190 LeuValAsnLeuAspGlyGluValIleGlyIleAsnThrLeuValThrAlaGlyIle 209
    |||||
Db 769 CTGGTGAACCTGGATGGCGAGGTCAATTGGCATCAACAGCTCAAGGTCAAGCTGGCATC 828
    |||||
Qy 210 SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGln 229
    |||||
Db 829 TCTTTGGCATCCCTTCAGACCGCATCAACGGTTCTTCACAGAGTTCAGAGACAGCAG 888
    |||||
Qy 230 IleLysAspTrpLysArgPheIleGlyIleArgMetArgThrIleThrProSerLeu 249
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Db 889 ATCAAA-----GCCCTCACTG 906
    |||||
Qy 250 ---ValAspGluLeuLysAlaSerAsnProAspPheProGluValSerSerGlyIleTyr 268
    |||||
Db 907 GCAGTTCAATTGAGAGCAGGGGCTTCTCAAGTTCCCTCCATGACCCCGTCAGC 966
    |||||
Qy 269 ValGlnGluValAlaProAsnSerPro-----SerGlnArg 280
    |||||
Db 967 CAAGCACTKGDACCCTCGTGCAGCCAGGCTGGTCCATGAGGGCTGTGCATGAAGA 1026
    |||||
Qy 281 GlyIleIleGlnAspGlyAspIleIleValLysValAsnGlyArgProLeu---ValAsp 299
    |||||
Db 1027 GCTGCTGTGAGAGATGCCCATTTGTTCTCTGTGT-----CCATTATGGGAGAGC 1077
    |||||
Qy 300 SerSerGluLeuGlnGluAlaValLeuThrGlu-----SerProLeuLeuLeu 315
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Db 1078 AATCTGAGCGCAGGAGCCTGTCTTCCCAAGAGCTGAAGTCTTCTCTTGG 1134
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Job time : 839 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OW protein - nucleic search, using frame_p2n model

Run on: February 21, 2006, 20:57:05 ; Search time 495 Seconds

(without alignments)
1432.363 Million cell updates/sec

Title: US-10-617-443B-2

Perfect score: 1679
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Scoring table:

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 7204323 seqs, 1061406715 residues

Total number of hits satisfying chosen parameters: 14408646

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-LOOPT=0 -LOOPTXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsbm62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:*

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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1482.5	88.3	2551	12	US-11-186-284-78
2	1034.5	61.6	1443	8	US-10-821-234-613
3	1034.5	61.6	1894	9	US-11-072-512-795
4	1034.5	61.6	2036	12	US-11-091-883-91

5	882	52.5	2476	12	US-11-183-914-23	Sequence 23, Appl
6	414	24.7	1497	8	US-10-467-657-2095	Sequence 2095, Ap
7	410	24.4	1425	12	US-11-098-686-9246	Sequence 9246, Ap
8	410	24.4	1457619	12	US-11-098-686-8739	Sequence 8739, Ap
9	360.5	21.5	1446	8	US-10-454-437-55	Sequence 55, Appl
10	347	20.7	3007	8	US-10-793-626-3848	Sequence 3848, Ap
11	347	20.7	3650	8	US-10-793-626-3756	Sequence 3756, Ap
12	335.5	20.0	1269	12	US-11-074-176-3	Sequence 3, Appl1
13	318	18.9	954	8	US-10-793-626-1823	Sequence 1823, Ap
14	282	16.8	908	8	US-10-750-185-32084	Sequence 32084, A
15	282	16.8	908	8	US-10-750-623-32084	Sequence 32084, A
16	260.5	15.5	1482	8	US-10-793-626-1831	Sequence 1831, Ap
17	260.5	15.5	3794	8	US-10-793-626-3705	Sequence 3705, Ap
18	230.5	13.7	4306	8	US-10-793-626-3538	Sequence 3538, Ap
19	192	11.4	3101	8	US-10-793-626-4209	Sequence 4209, Ap
20	162	9.6	1376	8	US-10-750-185-32073	Sequence 32073, A
21	162	9.6	1376	8	US-10-750-623-32073	Sequence 32073, A
22	143	8.5	200	12	US-11-098-686-3608	Sequence 3608, Ap
23	131.5	7.8	200	12	US-11-098-686-3609	Sequence 3609, Ap
24	128	7.6	1314	8	US-10-454-437-59	Sequence 59, Appl
25	122	7.3	3343	8	US-10-485-517-31	Sequence 31, Appl
26	117.5	7.0	2033	8	US-10-485-517-32	Sequence 32, Appl
27	117	7.0	1102	8	US-10-750-185-32074	Sequence 32074, A
28	117	7.0	1102	8	US-10-750-623-32074	Sequence 32074, A
29	115.5	6.9	2806	8	US-10-485-517-30	Sequence 30, Appl
30	110.5	6.6	6582	12	US-11-000-688-606	Sequence 606, App
31	105	6.3	8575	8	US-10-453-372-167	Sequence 167, App
32	103	6.1	1944	8	US-10-793-626-567	Sequence 567, App
33	103	6.1	3073	8	US-10-793-626-3483	Sequence 3483, App
34	103	6.1	3353	8	US-10-793-626-3481	Sequence 3481, App
35	100.5	6.0	1422	8	US-10-467-657-5977	Sequence 5977, App
36	100.5	6.0	1422	8	US-10-467-657-7517	Sequence 7517, App
37	100	6.0	14770	8	US-10-821-234-268	Sequence 268, App
38	99.5	5.9	849	8	US-10-793-626-363	Sequence 363, App
39	99.5	5.9	3189	8	US-10-793-626-3694	Sequence 3694, App
40	99	5.8	1283	8	US-10-821-234-348	Sequence 348, App
41	97.5	5.8	1329	12	US-11-098-686-10023	Sequence 10023, A
42	96.5	5.7	1809	8	US-10-467-657-5017	Sequence 5017, App
43	93	5.5	6999	8	US-10-453-372-169	Sequence 169, App
44	93	5.5	8160	8	US-10-453-372-113	Sequence 113, App
45	93	5.5	9668	8	US-10-453-372-135	Sequence 135, App

ALIGNMENTS

RESULT 1
US-11-186-284-78
; Sequence 78, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITL OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MP001-02922RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228

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	LENGTH: 2551
	TYPE: DNA
	ORGANISM: Homo Sapiens
	FEATURE:
	NAME/KEY: CDS
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	US-11-186-284-78
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	Score: 1482.50 Matches: 319
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	Best Local Similarity: 97.6% Mismatches: 6
	Query Match: 18.3% Indels: 7
	DB: 12 Gaps: 0
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DB	606 GGCTTCACACAGTGTAGACAGCCCGGCTCAAGTTCATTCATGTGACGTGTGGAG 6655
QY	30 Lys1Lea1ProAlaVal1Val1h1s1LeG1LhNpHeuArgh1sPProLeuPheG1YArg 49
DB	666 AAGATGCACACAGCCGTGTGCATATAGAGCTCTTCTTGAGACACCCGCTGTTGGCCG 7255
QY	50 AaPVal1ProLeuSerSerG1YserG1YpHe1LeMetSerGlu1AG1YLeu1Le1eThr 69
DB	726 AAGGTCCCCCTGTCCAGCGGTTCTGCTTCATGTGCAGAGGCGCGCTGATCATCACC 7855
QY	70 AaPVal1h1eVal1ValSerSerAaSerA1a1AProG1YArgG1NglNleuLy1ValGln 89
DB	786 AATGCCACATGGTGTCTCCAGCAACATGCTGCCCGGCGAGGACAGCATCAAGTGTGAC 8455
QY	90 LeuG1NserG1YAsPserTyrg1u1aThr1LeuYAsP1LeaP1Ys1YserAsP1Le 109
DB	846 CTACAGAAATGGGACCTCTATGAGGCGCACCATCAAGACATCAAGAAAGTGGACATT 9055
QY	110 AlAThrr1LeuY1Leh1sPProLy1YLy1YLeuProVal1LeuLeuLeuG1Yh1sSerAla 129
DB	906 GCCACCATCAAGATCCATCCCAAGAAAGACCTCCTGTGTGTGCTGGGTCACTGGCC 9655
QY	130 AaPLeuArGProG1YG1uPheVal1Ala1LeG1YserProPheAlaLeuG1NAsnThr 149
DB	966 GACCTGCGCGGT- GGGGAGTTTGGTGGCGCATGGAGT- CCTTCGCGCTACAGAAACA 1020
QY	150 Val1ThrrThnG1Y1LeValSerThr1aG1NArgG1uG1YArgG1uLeuG1YLeuArGAsp 169
DB	1024 GTGACAC- GGCATCTGT- AGCACTGCCAGCG- GAGGGCAGGAGGCTGGGCTCCGGAC 1085
QY	170 SerAsPMetAsP1Yr1Le- G1NthzAsPAla1Le1Le- AsnTYrg1YAsnSerG1Y1P 189
DB	1081 TCCGACATGAGCTACATCAACAGCGAGTGCATCATTCACATCAAGGAACTCGGGGGAC 1145
QY	188 rOleuVal1AsnLeuAsP1YG1uVal1LeG1Y1LeaSnThrLeuLy1Val1ThAlAG1Y 209
DB	1141 CACTGGTGAACCTGTGATGGAGAGTATGGCATCAACGCTCAAGAGTCAACGCGTGGCA 1205
QY	209 LeSerPheAla1LeProSerAsPArG1LeThzArgPheLeuThrG1uPheG1NAsP1YsG 229
DB	1201 TCTCTTTGCCATCCCTCCAGACCGATCAACAGGTTCTCAACAGATTCCAAGACAGC 1265
QY	229 h1LeLyAsP1Yr1Y1YLy1YArgPhe1LeG1Y1LeArgMetArGThr1LeThProSerL 249
DB	1261 AGATCAAAAGACTGTAAAGAGCGCTTCATCGGCAATAGGATGCGGAGATCAACAGCC 1322
QY	249 euVal1AsP1uLeuLy1As1As1AsPAsPAsPheProG1uVal1SerSerG1Y1LeTYrY 269
DB	1321 TGTGTGATAGCTGAAGGCGCAGCAACCGGACTTCCAGAGGGTCAAGAGTGGAAATTATG 1385
QY	269 a1G1Ngl1uVal1A1ProAsnSerProSerG1NArgG1YG1LeG1NAsPGLYAsP1Le1 289

Dd		1381	TGCAAGAGTTGGCCGAATTACCTTCTCAGAGAGCGGCATCCAGATGTGATCTCA	1444
Oy		289	IeVallyVsVaIaengIyaProleuValaspSerSergIuleIngluaIaValleut	309
Dd		1441	TCGTCAAGGTCACAAGCGCGCTCTTAGTGACTCAGAGACTGCAGAGGCCGTGCTGA	1500
Oy		309	hrgIusePrProleuLeuIngIulaIayArggIyAspaAspLeuLeumPheSerIlea	328
Dd		1501	CCAGAGTCTCTCTTAATGAGAGTGCGCGGGGAAACGACGACTCTTTCAGCANCG	1560
Oy		329	IaprogIuValImec 334	
Dd		1561	CACCTAGAGTGCTCATG 1577	
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		US-10-821-234-613		
		/ Sequence 613, Application US/10821234		
		/ Publication No. US2005025511A1		
		GENERAL INFORMATION:		
		APPLICANT: Labat, Ivan		
		APPLICANT: Seache-Crain, Birtic		
		APPLICANT: Andarman, Susan		
		APPLICANT: Tang, Y. Tom		
		TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia		
		FILE REFERENCE: 821A		
		CURRENT APPLICATION NUMBER: US/10/821,234		
		PRIOR FILING DATE: 2003-04-07		
		PRIOR APPLICATION NUMBER: US 60/462,047		
		NUMBER OF SEQ ID NOS: 1704		
		SOFTWARE: pc_seq_genes Version 1.0		
		SEQ ID NO 613		
		LENGTH: 1443		
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		US-10-821-234-613		
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				2
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Oy		24	IleAlaSpVaIvaIgIuIySiIleaIaProIaIaValIHISIIegIulePheLeuArg 43	
Dd		514	ATGGCGGAGCGTGTGAGAAGATCCCGCTCGGTGATTATCGAATTGTTTCGCAAG 573	
Oy		44	HieProIeuPheIyArghaenValProIeuSerSergIySergIyPheIImetSergIu 63	
Dd		574	CTTCCGTTTTCTMAAGAGAGGTGCCGGTGGCTAGTGGCTTATATGTGTTCGAA 633	
Oy		64	AlAgIYleuIeiIethraMaIahIsvaIaIseSerSaenSerIaIaIaProGIyArg 83	
Dd		634	GATGGACTATCTGTGCAAAATCCACGTGTGTGACCAAC-----AAG 675	
Oy		84	GInGlneUuIyVaIcInIeUnIaenGIyAspSerTyRGuaIathrIleIyAspIle 103	
Dd		676	CACCGGCTCAAAGTTGACGTGAAGAACGGTGCACCTTCGAAGCCAATAATCAAGAGTGTG 735	
Oy		104	AsgIyIySeSaSpIleIaIthrIleySIleHIsProuIySVyIVyIeuProValIeu 123	
Dd		736	GATGAGAAAGCAACATCGCATCTCATMAAATGACCAAGGCCAAGCTGCTGCTTG 795	
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Db      796 CTGCTGGCCGCTCTCAGAGCTGGCGGAGGTTGCTGTCATCGGAAGCCCG 855
Qy      144 PheAlaLeuGlnAenThValThrThrGlyIleValSerThrAlaGlnArgGluGlyArg 163
Db      856 TTTTCCCTTCAAAAACAGCTCCACCGGATCGTAGACCAACCCAGGAGCGCGCAAA 915
Qy      164 GluLeuGlyLeuArgAspSerSerPheMetAspTyrIleGlnThrAspAlaIleIleAsnTyr 183
Db      916 GAGCTGGGGCTCCGCACTCAGACATGAGCTACATCCAGACGCGCATCTCAACTAT 975
Qy      184 GlyAenSerGlyGlyProLeuValAsnLeuAspGlyGluValIleGlyIleAsnThrLeu 203
Db      976 GGAACCTGGGAGGCGCCGTTACTTAACCTGACGCGTGAAGTATGGAATTAACTTTG 1035
Qy      204 LysValThrAlaGlyIleSerPheAlaIleProSerAspArgIleThrArgPheLeuThr 223
Db      1036 AAGTGACAGCTGAGTATCTCTTCCAAATCCCATCTGATTAAGATTAAAGTTCTCTCAG 1095
Qy      224 GluPheGlnAspLysGlnIleLysAsp-----TPrLysLysArgPheIleGlyIle 240
Db      1096 GAGTCCCATGACCGACAGGCCAAAGAAAAGCCATCACCAAGAAAGATATATGATATC 1155
Qy      241 ArgMetArgThrIleThrProSerLeuValAspGlyLeuLysValSerAsnProAspPhe 260
Db      1156 CGAATGATGTCATCTACGCTCCAGCAAGCAAGCAAGCTGAAGACCGGACCGGACTTC 1215
Qy      261 ProGluValSerSerGlyIleTyrValGlnGluValAlaProAsnSerProSerGlnArg 280
Db      1216 CCAGACGATCTCAGAGCGCTATATTAATTGAAGTAATTCCTGATACCCACCAAGACT 1275
Qy      281 GlyGlyIleGlnAspGlyAspIleIleValLysValAsnGlyAspProLeuValAspSer 300
Db      1276 GGTGCTCTCAAGAAAACGACGTCATTAATCAACATCAAGTGAAGTCCGCTGCTCCGCC 1335
Qy      301 SerGluLeuGlnAlaValLeuThrGlnSerProLeuLeuLeuGluValAlaArgArgGly 320
Db      1336 AATGATGTCAGGAGCTGATTAAGGAAAGACCCCTGAACATGCTGCTCCGACGGGT 1395
Qy      321 AsnAspAspLeuLeuPheSerIleAlaProGluValVal 333
Db      1396 AATGAATATCATCATGATCAAGTGAATCCCGAAGAAATT 1434

RESULT 3
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; Sequence 795, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUKUO
; APPLICANT: HIO, YUKI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOKU
; APPLICANT: OTSUKA, MOTOTOKU
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072, 512
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350, 978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
```

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; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 795
; LENGTH: 1894
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-512-795

Alignment Scores:
Pred. No.: 3,89e-114 Length: 1894
Score: 1034.50 Matches: 206
Percent Similarity: 80.2% Conservative: 61
Best Local Similarity: 61.9% Mismatches: 57
Query Match: 61.6% Indels: 10
Dels: 9 Gaps: 2

US-10-617-443b-2 (1-334) x US-11-072-512-795 (1-1894)

Qy      4 AlaLeuProAlaSerAlaGlyLeuHisGlnLeuSerSerProArgTyrLysPheAsnPhe 23
Db      358 GCGAGGCTGGCGGCCAAGGCGAG-GAAGATCCCAAGATTGGCCATTAATATATATCTTT 416
Qy      24 IleAlaAspValAlaGluLysIleAlaProAlaValAlaHisIleGluLeuPheLeuArg 43
Db      417 ATCCGGAGCGTGTGAGAAAGATGCGCCCTCGCGTTCATATGAAATTGTTTCGAAG 476
Qy      44 HisProLeuPheGlyArgAsnValProLeuSerSerGlySerGlyPheIleMetSerGlu 63
Db      477 CTTCGGTTTCTAAACGAGAGGTGCGGTGCTGATGTGGTCTGTGGTTATATGTGCGAA 536
Qy      64 AlaGlyLeuIleIleThrAsnAlaHisValValSerSerAsnSerAlaAlaProGlyArg 83
Db      537 GATGACATGATGTGACAAATGCCCCACGTGATGACCAAC-----AAG 578
Qy      84 GlnGlnLeuLysValGlnLeuGlnAsnGlyAspSerTyrGluAlaThrIleLysAspIle 103
Db      579 CACCGGCTCAAAAGTTGAAGCTGAAGAACGTGTGCACTTAAGAAAGCAAAATCAAGATGTG 638
Qy      104 AspLysLysSerAspIleAlaThrIleLysIleHisProLysLysLysLeuProValLeu 123
Db      639 GATGAAGAAAGACAGATGCACTCAATTAATTAACCAACAGGGCAAGCTGCTGTCTCG 698
Qy      124 LeuLeuGlyHisSerAlaAspLeuArgProGlyGluPheValAlaIleGlySerPro 143
Db      699 CTGCTGGCCGCTCTCAGAGCTGGCGGAGAGTTGCTGCTGCTCCATCGGAAGCCCG 758
Qy      144 PheAlaLeuGlnAenThValThrThrGlyIleValSerThrAlaGlnArgGluGlyArg 163
Db      759 TTTTCCCTTCAAAAACAGCTCCACCGGATCGTAGACCAACCCAGGAGCGCGCAAA 818
Qy      164 GluLeuGlyLeuArgAspSerSerPheMetAspTyrIleGlnThrAspAlaIleIleAsnTyr 183
Db      819 GAGCTGGGGCTCCGCACTCAGACATGAGCTACATCCACGACGAGCCCATCATCAACTAT 878
Qy      184 GlyAenSerGlyGlyProLeuValAsnLeuAspGlyGluValIleGlyIleAsnThrLeu 203
Db      879 GGAACCTGGGAGGCGCCGTTAGTAACCTGAGCGGTGAAGTGAATTGAATTAACTTTG 938
Qy      204 LysValThrAlaGlyIleSerPheAlaIleProSerAspArgIleThrArgPheLeuThr 223
Db      939 AAGTGACAGCTGGAATCTCTTTCATCCCATCTGATTAAGATTAAAGTTCTCTCAG 998
Qy      224 GluPheGlnAspLysGlnIleLysAsp-----TPrLysLysArgPheIleGlyIle 240
Db      999 GAGTCCCATGACCGCAGAGCCAAAGAAAAGCCATCACCAAGAAAGATATATGATATC 1058
Qy      241 ArgMetArgThrIleThrProSerLeuValAspGlyLeuLysValSerAsnProAspPhe 260
Db      1059 CGAATGATGTCATCTACGCTCCAGCAAGCAAGAGCTGAAGAGACCGGACCGGACTTC 1118
Qy      261 ProGluValSerSerGlyIleTyrValGlnGluValAlaProAsnSerProSerGlnArg 280
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Db 1119 CCAAGCGGATCTCAGGAGCGGTATTAATTGAAGTAATTCCTGATACCCACGAGAAAGCT 1178
 QY 281 G|G|G|Y|I|E|G|I|A|S|P|G|I|A|S|P|I|E|V|A|L|S|V|A|A|N|G|I|A|T|G|P|R|O|L|E|U|V|A|A|S|P|S| 300
 Db 1179 GGTGGTCTCAAGAAAACGACGTCATATACAGCATCATGTGACAGTCGTGTCTTCGCC 1238
 QY 301 S|E|T|G|L|E|U|G|I|N|G|I|V|A|L|V|A|L|E|U|T|H|R|G|L|U|S|E|R|P|R|O|L|E|U|L|E|U|G|I|V|A|L|A|T|G|I| 320
 Db 1239 AATGATGTCACGACGTCATTAAAAAGGAAAAACACCCCTGAACATGTGTGTGTCGACGAGGCT 1298
 QY 321 A|A|N|A|S|P|L|E|U|L|E|U|P|H|E|S|E|R|I|E|L|A|P|R|O|G|I|V|A|L|V|A|L| 333
 Db 1299 AATGAGATATCATGATCATCATGATGTTCCCGAAGAAAT 1337

RESULT 4

```

Sequence 91 Application US/11,091,883
Publication No. US20060024693A1
GENERAL INFORMATION:
APPLICANT: CIBELTI, JOSE
APPLICANT: FERNANDEZ, EMILIO O.
APPLICANT: JORDAO DE MEGALHAES, GUILHERME
APPLICANT: KOCABAS, ARIF
APPLICANT: CROSBY, JAVIER A.
TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH
TITLE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEONORNAL
TITLE OF INVENTION: VIABILITY
FILE REFERENCE: 3594205
CURRENT APPLICATION NUMBER: US/11/091,883
CURRENT FILING DATE: 2005-03-29
PRIOR APPLICATION NUMBER: 60/556,875
PRIOR FILING DATE: 2004-03-29
NUMBER OF SEQ ID NOS: 513
SOFTWARE: PatentIn version 3.3
SEQ ID NO 91
LENGTH: 2036
TYPE: DNA
ORGANISM: Homo sapiens
IS-11-091-883-91

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Alignment Scores:

Pred. No.:	4.27e-114	Length:	2036
Score:	1034.20	Matches:	61
Percent Similarity:	80.2%	Conservative:	206
Best Local Similarity:	61.9%	Mismatches:	57
Query Match:	61.6%	Indels:	10
DB:	12	Gaps:	2

US-10-617-443B-2 (1-334) X US-11-091-883-91 (1-2036)

[illegible]

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QY      124  LeuLeuGlyYH1sSerAlaAspLeuArgProGlyGluPheValValAlIleGlySerPro 143
DB      844  CTGCTGGCCCGCTCCTCAAGCTGGCGGCCGGAGAGTTCTGAGTCCGCATCGGAAGCCG 903
QY      144  PheAlaLeuGlnAsnThrValThrThrGlyIleValSerThrAlaGlnArgGluIArg 163
DB      904  TTTTCTCTTCAAAACACAGTACACCACGGAGATCGTAGACACACACCGAGCGAGCANA 963
QY      164  GluLeuGlyLeuArgAspSerAspMetAspTrpIleGlnThrAspAlaIleIleAsnTrp 183
DB      964  GAGCTGGGGGCTCCCGCAACTCAGACATGAGCTATCACTTCAGACCGACGCACTCATCAAT 1022
QY      184  GlyAsnSerGlyGlyProLeuValAsnLeuAspGlyGluValIleGlyIleAsnThrLeu 203
DB      1024  GGAATCTGGGAGAGCGCCCTTAGTAACTCGAGCGGTGAAGTATTGAACTTACCTTTG 1084
QY      204  LysValThrAlaGlyIleSerPheAlaIleProSerAspArgGlyThrArgPheLeuThr 223
DB      1084  AAAGTGACAGCTGGAATCTCTTTGCATCTCCATCTGATTAAGTAAATAAAGTTCTTCA 1144
QY      224  GluPheGlnAspLysGlnIleLeuAsp-----TrpLysLysArgPheIleGlyIle 240
DB      1144  GAGTCCCATGACCGACGACGACGCAAGGAAAGAACCATCAACCAAGAAAGATATATGTG 1203
QY      241  ArgMetArgThrIleThrProSerLeuValAspGluLeuLysAlaSerAsnProAspPhe 260
DB      1204  CGAATGATGATCACTCACTCACTCCAGCAAGAACCAAGAGCTGAAGAGACCGGACCTTC 1266
QY      261  ProGluValSerSerGlyIleTrpValGlnGluValAlaProAsnSerProSerGlnArg 280
DB      1264  CCAGACCGTGAATCTCAGAGCGCTATATATTAATTAAGAAATTTCTGATTAACCCAGCA 1322
QY      281  GlyGlyIleGlnAspGlyAspIleIleValLysValAsnGlyArgProLeuValAspSer 300
DB      1324  GGTGGTCTCAAGAAACGACGCTATATATGACATCAATGAGCAAGTCCGTGGTCTCCGCC 1383
QY      301  SerGluGlnGlnGluAlaValLeuThrGluSerProLeuLeuGluValAlaArgGly 320
DB      1384  AATGATGTCACGACGACGCTATTMAAGAAAGAACACCTCGAACAATGTGGTCCGAGGGCT 1444
QY      321  AsnAspAspLeuLeuPheSerIleAlaProGluValVal 333
DB      1444  AATGAAGTATCATGATCATCAAGTATTCGCCGAATAATT 1482

RESULT 5
US-11-183-914-23
; Sequence 23, Application US/11183914
; Publication No. US20050282214A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Tang, Tom Y.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSD for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/183,914

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RESULT 5

US-11-183-914-23

; Sequence 23, Application US/11183914
; Publication No. US20050282214A1

GENERAL INFORMATION

APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L

APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.

APPLICANT: Corley, Neil C.
APPLICANT: Tang, Tom Y.
APPLICANT: Chab, David

APPLICANT: SHAH, FOLVI
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 34

NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc

STREET: 3174 Porter Dr.
CITY: Palo Alto

STATE: CA
COUNTRY: USA

ZIP: 94304
COMPUTER READABLE

```
; MEDIUM TYPE: Diskette
;
; COMPUTER: IBM Compatible
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; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/183,914

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FILING DATE: 19-JULY-2005
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SINITUCTOI
CLONE: 2680548
US-11-183-914-23

Alignment Scores:
Pred. No.: 1,378-95 Length: 2476
Score: 882.00 Matches: 169
Percent Similarity: 74.84 Conservative: 72
Best Local Similarity: 52.54 Mismatches: 71
Query Match: 52.54 Indels: 10
DB: 12 Gaps: 2

US-10-617-443B-2 (1-334) x US-11-183-914-23 (1-2476)
QY 15 SerSerProArgTyLysePheAsnPhelIeAlaAspValValGluValIleAlaProAla 34
DB 481 GCTTCTCCCGAGTCAGTACACTTCAATCGAGATGATGATGAGAGAAGACGACCTCC 540
QY 35 VALVALHsIleGluLeuPheLeuArgHsPProLeuPheGlyArgAsnValProLeuSer 54
DB 541 GTGGCTATATCGAATCTGAGCCGCCCTCTTCTGGGCGGAGGTCCTATCTCG 600
QY 55 SerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThrAsnAlaHsValVal 74
DB 601 AACGCTCAGGATTTGATGCTGCTCCAGATGCTCATTTGTACCAACGCCCATGTGGTG 660
QY 75 SerSerAsnSerAlaAlaProGlyArgGlnGlnLeuValGlnLeuGlnAsnGlyAsp 94
DB 661 GCTGAT-----CGGCCAGAGTCCGCTGAGACTGCTAAGCGGCAC 702
QY 95 SerTyrgluAlaThrIleLysAspIleAspLysSerAspIleAlaThrIleLysIle 114
DB 703 ACGTATGAGGCCGCTGTCACAGCTGATCCCGTGGCAGACATCGCAACGCTGAGAT 762
QY 115 HsPProLysLysLeuProValLeuLeuLeuGlyHsSerAlaAspLeuArgProGly 134
DB 763 CAGACTAAGAGACCTCTCCCAACGCTGCTGGAGCGCTGATGATCGGAGAGGG 822
QY 135 GluPheValValAlaIleGlySerProPheAlaLeuGlnAsnThrValThrThrGlyIle 154
DB 823 GAGTTTGTGTTGCCATGGAGATCCCTTTGCATCGCAGAACATCATCCGCGCAT 882
QY 155 ValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAspSerAspMetAspTy 174
DB 883 GTTACTCGCTCAGCTCAGCTCAGACAGACCTGGAGCTCCCAACCAATGTGAATAC 942
QY 175 IleglnThrAspAlaIleIleAsnTyrgLysAsnSerGlyGlyProLeuValAsnLeuSer 194
DB 943 ATTCAACTGATGAGCTATTTATTTTGAACCTGGAGGTCCTCGTTAACTGAT 1002
QY 195 GlyGluValIleGlyIleAsnThrLeuLysValThrAlaGlyIleSerPheAlaIlePro 214

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DB 1003 GGGAGGTGATTGGATGTGACACCATGAGGTCAAGCTGGAATCTCTTGGCATCCCT 1062
QY 215 SerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGln-----Ile 230
DB 1063 TCTGATCTCTTCGAGAGATTTCTGATCTGTGGGAAAAAGAAATTCCTCTCCGGAATC 1122
QY 231 LysAspTrpLysLysArgPheIleGlyIleArgMetArgThrIleThrProSerLeuVal 250
DB 1123 AGTGGTCCAGCGCGGCTACATTTGGGGTATGATGTGACCTCGAGTCCAGCATCTCT 1182
QY 251 AspGluLeuLysAlaSerAsnProAspPheProGluValSerSerGlyIleTyValGln 270
DB 1183 GCTGAATACACGCTTTCAGAACCAAGCTTCCCATATTCAGCATGTGGTGTCTCAT 1242
QY 271 GluValAlaProAsnSerProSerGluArgGlyGlyIleGlnAspGlyAspIleIleVal 290
DB 1243 AAGTCATCTGGGCTCCCTCGACACCGGGCTGTGTGGCGCTGGAGTGTATTTTG 1302
QY 291 LysValAsnGlyArgProLeuValAspSerSerGluLeuGlnGluValAlaLeuThrGlu 310
DB 1303 GCCATGGGAGAGCAGATGTGTAACAAATGCTGAAGATTTTATGAAGCTTTGAAACCAA 1362
QY 311 SerProLeuLeuLeuGluValArgArgGlyLysAsnAspLeuLeuPheSerIleAlaPro 330
DB 1363 TCCAGTTGGCAGTGCAGATCCGGCGGGAGCAGAAACATGACCTTATATGTGACCCCT 1422
QY 331 GluVal 332
DB 1423 GAGGTC 1428

RESULT 6
US-10-467-657-2095
Sequence 2095, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASTIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
PRIOR FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: Seqwin99, version 1.04
SEQ ID NO 2095
LENGTH: 1497
TYPE: DNA
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2095

Alignment Scores:
Pred. No.: 2,056-39 Length: 1497
Score: 414.00 Matches: 112
Percent Similarity: 51.24 Conservative: 58
Best Local Similarity: 33.74 Mismatches: 98
Query Match: 24.74 Indels: 64
DB: 8 Gaps: 10

US-10-617-443B-2 (1-334) x US-10-467-657-2095 (1-1497)
QY 25 AlaAspValValGluValIleAlaProAlaValAlaHsIleGluLeu----- 40
DB 172 GCCCAACTGTTCAAAAGGAAGGCCCGGCACTGTCATATTACGAGCCGCCGCCG 231
QY 40 ----- 40
DB 232 CGCACCCAAAACGGCAGCGGCAATGCCGAAACCAATTCGACCCGCTTGGCAGACGAC 291
QY 41 ---PheLeuArgHsPProLeuPheGlyArgAsnValPro----- 52

```

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Db 292 CCGTTC-----TACGATTTTCAACGCGCTGTCCTCCGACATGCCCGAAATCCCCCA 345
Qy 53 -----LeuSerSerGlySerGlyPheIleMetSerGluAlaGly 65
Db 346 GAAGAAGACAGATGACGGCGGATTTGAATTCGCGGCTTCATCATGACAAACCGCG 405
Qy 66 LeuIleIleThrAsnAlaHisValValSerSerAsnSerAlaAlaProGlyArgGlnGln 85
Db 406 TACATCTGACCAATACCCACGTCGTGTC-----GGATGGGCACT 447
Qy 86 LeuIleValGlnLeuGlnAsnGlyAspSerTyrgLysAlaThrIleLysAspIleAspLys 105
Db 448 ATCAAAAGTCCTGCTGCAACGACGCGGAAATATACGCCAAATCATCGGTCGATGTC 507
Qy 106 LysSerAspIleAlaThrIleLysIleHisProLysLysLysLeuProValLeuLeuLeu 125
Db 508 CAATCCGATGTCGCTTCGAAATCGACGCAACGGAAGAGCTACCCGTCGTCAAAATC 567
Qy 126 GlyHisSerAlaAspLeuArgProGlyGlnPheValAlaIleGlySerProPheAla 145
Db 568 GGAATATCCCAAAATTTGAAACCGGCGAATGGGTGCTGCTGCAATCGGCGGCTTCGCGC 627
Qy 146 LeuGlnAsnThrValThrThrGlyIleValSerThrAlaGlnArgGlnArgGlnLeu 165
Db 628 TTGACACACAGCGTGACCGCGCGCATCGTGTCCGCC-----AAAGCAGAAAGCTTG 678
Qy 166 GlyLeuArgAspSerAspMetAspTyrlIleGlnThrAspAlaIleIleAsnTyrgLysAn 185
Db 679 CCC---AACGAAAGCTACACACCCCTTCATCCAAACGACGTTGCTCCATCATCGGCGCAAT 735
Qy 186 SerGlyGlyProLeuValAsnLeuAspGlyGlnValIleGlyIleAsnThrLeuLysVal 205
Db 736 TCCGGGCGGCGCTGTTCAACTTAAAGACAGGTGTGCGCATCAATTCGCAAAATATAC 795
Qy 206 Thr-----AlaGlyIleSerPheAlaIleProSerAspArgIleThrArg 220
Db 796 AGCGGACGAGCGGATTCATGCGCATCTCTTGCCATCCGATTCAC---GTTCGCATG 852
Qy 221 PheLeuThrGluPheGlnAspLysGlnIleLysAspTrpLysArgPheIleGlyIle 240
Db 853 AATGTGCGGAA---CAGCTGAAACAAACCGCGCAAGTCCACGCGACAACTGGGCGATG 909
Qy 241 ArgMetArgThrIleThrProSerLeuValAspGluLeuLysAlaSerAsnProAspPhe 260
Db 910 ATTATTCAGAAAGATTCCTACGCTTGGCACAGCTCGTGGCTG----- 954
Qy 261 ProGluValSerSerGlyIleTyrgValGlnGluValAlaProAsnSerProSerGlnArg 280
Db 955 ---GATTAAGCCAGCGCGCATGATGCAAAATCTTCCGCGGACGCCCGCAGAAAGCT 1011
Qy 281 GlyGlyIleGlnAspGlyAspIleIleValLysValAsnGlyArgProLeuValAspSer 300
Db 1012 GCGGCGCTCAAGCGCGGCGACATGTCCTCAGCTGACGCGGAGAAATACGTTCTTCC 1071
Qy 301 SerGluLeuGlnGluValLeuThrGluSerPro 312
Db 1072 GCGGACCTTCCTCATGCTGCGCGCATTAACGCCG 1107

RESULT 7
US-11-098-686-9246
; Sequence 9246, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND PEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
```

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; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9246
; LENGTH: 1425
; TYPE: DNA
; ORGANISM: Lawsonia intracellularis
US-11-098-686-9246

Alignment Scores:
Pred. No.: 5,846-39 Length: 1425
Score: 410.00 Matches: 94
Percent Similarity: 57.4% Conservative: 58
Best Local Similarity: 35.5% Mismatches: 89
Query Match: 24.4% Indels: 24
DB: 12 Gaps: 7

US-10-617-443B-2 (1-334) x US-11-098-686-9246 (1-1425)

Qy 54 SerSerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThrAsnAlaHisVal 73
Db 271 TCATTAGAACTGCTTTTATCATTTCTTCAGATGATATATTGTTACCAATATATATGTG 330
Qy 74 ValSerSerAsnSerAlaAlaProGlyArgGlnGlnLeuLysValGlnLeuGln----- 91
Db 331 ATAGAA-----GGACAGATTCGTGTAAGTAATCTTGAAAGTACC 372
Qy 92 -----AsnGlyAspSerTyrgLysAlaThrIleLysAspIleAspLysSerAspIle 109
Db 373 TCAGCAAAAGAAATCTACCTGACAGAGATGATAGTAAAGATGAAGAAACAGATCTT 432
Qy 110 AlaThrIleLysIleHisProLysLysLysLeuProValLeuLeuGlnGlyHisSerAla 129
Db 433 GCTTATTATTAAGTTAAAGTAAGATCATCTACTTATTCTTATTTGGAAATTCAGAT 492
Qy 130 AspLeuArgProGlyGlnPheValValAlaIleGlySerProPheAlaLeuGlnAsnThr 149
Db 493 ACTATGAAAGTTGGATGATGGTGTGCTACCTATTGGTAATCTTTGGCTTAGGCCATACA 552
Qy 150 ValThrThrGlyIleValSerThrAlaGlnArgGlnArgGlnLeuLysAsp 169
Db 553 GTTACAGACGATATATTAAGTCT-----AAAGCAGATTCATTCATGCTGGACCA 603
Qy 170 SerAspMetAspTyrlIleGlnThrAspAlaIleIleAsnTyrgLysAsnSerGlyPro 189
Db 604 TTTGAT---AATTTTCAAACTGATCATCTATCATCTCGGGAATATAGTGTGTTCCA 660
Qy 190 LeuValAsnLeuAspGlyGlnValIleGlyIleAsnThrLeuLysValThrAla----- 207
Db 661 TTAATCAATATGTCAAGCAAGTTGTAGCATTTAAACACAGCTATTATATGCAAGTGGCNA 720
Qy 208 GlyIleSerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAsp 227
Db 721 GGTATTTGTTTCGCTATCCCAAGTAGTATGCGACATCTATTATTAAGACAGTTA----- 774
Qy 228 LysGlnIleLysAspTrpLysLysArgPheIleGlyIleArgMetArgThrIleThrPro 247
Db 775 AAGACAATTAAGTAAGTAAGAGCTGATAGTGAACAATTCAAGATGATGATCT 834
Qy 248 SerLeuValAspGluLeuLysAlaSerAsnProAspPheProGluValSerSerGlyIle 267
Db 835 AATACAGCTAAAGCTTGAGATTATCTCAG-----GCAAAAGTCCG 876
Qy 268 TyrValGlnGluValAlaProAsnSerProSerGlnArgGlyIleGlnAspGlyAsp 287
Db 877 CTTGAGGTTCTGTTGTTCTCGAGATCTGCTGTAAGGCTGCTTAAGATTGGCAT 936
Qy 288 IleIleValLysValAsnGlyArgProLeuValAspSerSerGluLeuGlnGlnValAla 307
Db 937 ATTGTAACAACAAGCTGATGTAACAATTAATGATGCAAGCTATTGTTAAACATATT 996
Qy 308 LeuThrGluSerPro 312
```

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Db      997 GCTACTAACTCTCT 1011
RESULT 8
US-11-098-686-8739/c
; Sequence 8739, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT FILING DATE: 2005-04-04
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8739
; LENGTH: 1457619
; TYPE: DNA
; ORGANISM: Lawsonia intracellularis
US-11-098-686-8739

Alignment Scores:
Pred. No.:      4,42e-35      Length:      1457619
Score:          410.00      Matches:      94
Percent Similarity: 57.4%      Conservative: 58
Best Local Similarity: 35.5%      Mismatches: 89
Query Match:    24.4%      Indels:      24
                Gaps:      7

US-10-617-443B-2 (1-334) x US-11-098-686-8739 (1-1457619)
QY      54 SerSerGlySerGlyPheIleMeSerGluAlaGlyLeuIleIleThrAsnAlaHisVal 73
      434347 TCATTAGGAGACGCTTTATCATCTTTCAGATGATATATGTTACCAATATCATGTG 434288
      74 ValSerSerAsnSerAlaAlaProGlyArgGlnGlnLeuValGlnLeuGln----- 91
      434287 ATAGAA-----CGAGCAGATCTCTGTTAGAGTAATCTTGAAAGTACC 434246
QY      92 -----AangLyAspSerTyrgLualarhrielysaApIleAspLybysSerAspIle 109
      434245 TCAGGCAAGAAAGATCACTACCTGACAGAGTACGATGAGTGAAGAAACAAATCTT 434186
QY      110 AlaThrIleValIleHisProLySylsLeuProValIleuLeuGlyHisSerAla 129
      434185 GCTTATTAAAGTTAAAGTAAAGTAAAGTCACTTATCTTATATTGGAATTCACAGT 434126
QY      130 AspLeuArgProGlyGluPheValAlaIleGlySerProPheAlaLeuGlnAsnThr 149
      434125 ACTATGGAAGTTGGTGAATGGGTGCTAGCTATTGCTTAATCTTTGGGTAGCCATACA 434066
QY      150 ValThrThrGlyIleValSerThrAlaGlnArgGluGlyArgGlnLeuGlyLeuArgAsp 169
      434065 GTTACAGACGATATTAAGTCT-----AAAGACGATATTCATGCTGACCA 434015
QY      170 SerAspMetAspTyrgIleGlnThrAspAlaIleIleAsnTyrgIAsnSerGlyLyPro 189
      434014 TTTGAT---AAGTTTAAACATGATGATCATCATCAATCCGGGAATAGTGTGTCCA 433958
QY      190 LeuValAsnLeuAspGlyGluValIleGlyIleAsnThrLeuValThrAla----- 207
      433957 TTAATCAATATGTCAGGACAAAGTTGATGACATTAACACAGCTATATATGCAAGTGGCA 433898
QY      208 GlyIleSerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAsp 227
      433897 GGTATTGGTTTCGCTATCCCAAGTATGATGCAAGATCGATATTAATAGACAGTTA----- 433844
QY      228 LysGlnIleLeuAspTrpLyLeuArgPheIleGlyIleArgMetArgThrIleThrPro 247
      228 LysGlnIleLeuAspTrpLyLeuArgPheIleGlyIleArgMetArgThrIleThrPro 247

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Db      433843 AAGACAATTAAGAGTAAGTAGGTGATGATGTAACAAATTCAGAGATGATACT 433784
QY      248 SerLeuValAspGluLeuValAlaSerAsnProAspPheProGluValSerSerGlyIle 267
      433783 AATACAGCTAAAGCTCTGTGATTAATCTCAG-----GCATAAGGTGCG 433742
QY      268 TyrValGlnGluValAlaProAsnSerProSerGlnArgGlyIleGlnAspGlyAsp 287
      433741 CTTGATGTTCTGTTCTTCTCGAGATCTGCTGATTAAGGCTGTTAAAGTGGCAT 433682
QY      288 IleIleValLyValAsnGlyArgProLeuValAspSerSerGlyLeuGlnGluAlaVal 307
      433681 ATTGTACCAACAGCTGATGTAACAAATGTAGTGAAGCTCATTTGTAAGACTAAT 433622
QY      308 LeuThrGluSerPro 312
      433621 GCTACTAACTCTCT 433607
Db      433621 GCTACTAACTCTCT 433607
RESULT 9
US-10-454-437-55
; Sequence 55, Application US/10454437
; Publication No. US20050277115A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroeger, Burkhard
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberkner, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; FILE REFERENCE: BGI-128PCPN
; CURRENT FILING DATE: 2003-06-13
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 55
; LENGTH: 1446
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1423)
; OTHER INFORMATION: RXA02630
US-10-454-437-55

Alignment Scores:
Pred. No.:      5.57e-33      Length:      1446
Score:          360.50      Matches:      101
Percent Similarity: 49.5%      Conservative: 44
Best Local Similarity: 34.5%      Mismatches: 97
Query Match:    21.5%      Indels:      51
                Gaps:      9

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US-10-617-443B-2 (1-334) x US-10-454-437-55 (1-1446)

QY 27 ValValaGluLysIleAlaProAlaValaValHisIleGluLeuPheLeuArgHisProLeu 46
 536 GTTGGCGCGAGCTTTGCTTCTGCTCTATTCAGCGCATTAAGT----- 586

QY 47 PheGlyArgAsnValProLeuSerSerGlySerGlyPheIleMetSerGluValaGlyLeu 66
 587 -----ACGTCTGCTCTGAGGCTCTGATCCATTAATTTCTCGATGCTTAC 634

QY 67 IleIleThrAsnAlaHisValaValSerSerAsnSerAlaAlaProGlyArgGln----- 85
 635 GTCATGACCAATATACGCTCGTGCA-----GGCATTTAACAACTCT 676

QY 86 -----LeuLysValGluLeuGlnAsnGlyAspSerTyrGluAlaThrIleLysAspIle 103
 677 GGTGTGTAGAAAGTATGTTCTCCGATGAACTACAGCCAAAGCTATTTATTCCTGT 736

QY 104 AspLysLysSerAspIleAlaThrIleLysIleHisProLysLysLeuProValLeu 123
 737 GATCCTTCCACAGATATTGCTGTGATCAAGATTAGGATGTGTCCAACCTTCAGTTTATG 796

QY 124 LeuLeuGlyHisSerAlaAspLeuArgProGlyGluPheValValaIleGlySerPro 143
 797 AGCTTGGAGATTCCGACGCAATAGCGTTGACAAAGTGTGATGAGCTGTGTTCTCCA 856

QY 144 PheAlaLeuGlnAsnThrValThrThrGlyIleValSerThrAlaGlnArgGluArg 163
 857 CTGGGTTGAGCTTCCACTGTGACACCGGATATTGTGTGGCGCGTGAACGCTCTGTCGA 916

QY 164 GluLeu-----GlyLeuArgAspSerAspMetAspTyrIleGlnThrAspAlaIle 181
 917 GCTTCTGTGATGGCGAGAGTCTGCTCATCATGCTTATCCAGACCGATGCTGGATC 976

QY 182 AsnTyrGlyAsnSerGlyGlyProLeuValAsnLeuAspGlyGluValIleGlyIleAsn 201
 977 AACCTGCTAATCTGTGTGTGCTGCTGCTGATGATGATGCAACCTCATTTGGCATGAAT 1036

QY 202 ThrLeuLysVal-----ThrAlaGlyIleSerPhe 211
 1037 TCGGTAAATTCGATTCGATTCGAGCAGCAGCATTCGCGAGTTCCTGATTTGCTGTTT 1096

QY 212 AlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGlnIleLys 231
 1097 TCTATCCCATCCAC-----TTTCCCAAGCCGCGCGCATTCATATGATCAGC 1144

QY 232 AspTrpLys-----LysArgPheIleGlyIleArgMetArgThrIleProSerLeu 249
 1145 ACCGGCCAGTAACTACGCGCATGATCGGTGCGAGTGTGGCACT----- 1189

QY 250 ValAspGluLeuLysAlaSerAsnProAspPheProGlyValSerSerGlyIleTyrVal 269
 1190 -----GACAATCAATGACACGCGCTGTATTT 1216

QY 270 GlnGluValAlaProAsnSerProSerGlnArgGlyGlyIleGlnAspGlyAspIleIle 289
 1217 GCCAGTGTTCAGAGTGTGACCGCGCGAGATGCTGACCTTCAGCCAGCGATATCGTG 1276

QY 290 ValLysValaAsnGlyArgProLeuValaAspSerSerGlu 302
 1277 ACCAAGCTCAATGATCGA---GTATGATAGCCCGAC 1312

DB 1277 ACCAAGCTCAATGATCGA---GTATGATAGCCCGAC 1312

RESULT 10
 US-10-793-626-3848
 ; Sequence 3848, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMBERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PUI480US
 ; CURRENT APPLICATION NUMBER: US/10/793,626
 ; CURRENT FILING DATE: 2004-03-04
 ; PRIOR APPLICATION NUMBER: 60/164,258

PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3848
 ; LENGTH: 3007
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: nucleic acid sequence
 US-10-793-626-3848

Alignment Scores:
 Pred. NO.: 6,08e-31 Length: 3007
 Score: 347.00 Matches: 94
 Percent Similarity: 50.9% Conservative: 72
 Best Local Similarity: 28.8% Mismatches: 104
 Query Match: 20.7% Indels: 56
 DB: Gaps: 11

US-10-617-443B-2 (1-334) x US-10-793-626-3848 (1-3007)

QY 8 SerAlaGlyLeuHisGlnLeuSerSerProArgTyrLysPheAsnPheIleAlaAspVal 27
 56 AGTCATGTGCGCAATCATGTTAGATGTGTAAGTAATCAATCAATCAATCAATGATG 115

QY 28 ValGluLysIleAlaProAlaValaValHisIle----- 38
 116 ATTAAGACGTTTCTCCGCAATTTGCGCGTATTAACATGCAAAATCTACAACTT 175

QY 39 ---GluLeuPheLeuArgHisProLeuPheGlyArgAsnValProLeuSerSerGlySer 57
 176 GATGATTTATTCAACCGTAAAGCATTTAATCAAAAGAGCGGAATTTGTTCCGCTGTG 235

QY 58 GlyPheIleMetSerGlu---AlaGlyLeuIleIleThrAsnAlaHisValaValSerSer 76
 236 ATTTATCAAAATTAAGTAAGTTCGCCATATATCGTTCAAAATTAATCAAGTGTGAT-- 292

QY 77 AsnSerAlaAlaProGlyArgGlnGlnLeuLysValGlnLeuGlnAsnGlyAspSerTyr 96
 293 -----GGTCTCTCGGAATTAAGTTCAACTCAATTAATTCAAACCAAGTA 337

QY 97 GluAlaThrIleLysAspIleAspLysLysSerAspIleAlaThrIleLysIleHisPro 116
 338 GATGCCAAATTAATAGTAAAGACCCCTAACAGATATTGCTGTTCAAAATTAAGAT 397

QY 117 LysLysLysLeuProValaLeuLeuLeuGlyHisSerAlaAspLeuArgProGlyGluPhe 136
 398 ACAAAGGAATTAAGCAATTCATTTGCTAATTCGTCAAAAGTTCAAAACAGAGATAGT 457

QY 137 ValValaIleIleGlySerProPheAlaLeuGln-----AsnThrValThrThrGlyIle 154
 458 GTTTTTCAGATGGTAAATCTCTAGGATTAAGAAATTCGAAATTCGTTATCATCAGGAAT 517

QY 155 ValSerThrAlaGlnArgGlu---GlyArgGluLeuGlyLeuArgAspSerAspMetAsp 173
 518 ATTTCAGCTAGCAAGCAATTAATGACGCCAATTAATCTCTGCTGTAATCTAAAGTTAAT 577

QY 174 TyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyProLeuValaAsnLeu 193
 578 GTTTTTCAGACACACGCTGCAATTAATCCCGGTAATTCGGGTGCTGATTAAGGATAT 637

QY 194 AspGlyGluValaIleGlyIleAsnThrLeuLysValaThrAla-----GlyIle 209
 638 AACGGAATCTCGTTGATTCATTCATGCAATTAATGCGGACGACCAAGTAGAAGTATA 697

QY 210 SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGln 229
 698 GGTTCCTAATCTACTAATTAAGTGAAGTACCACT-----GAACAATCT 745

QY 230 IleLysAspTrpLys-----LysArgPheIleGlyIleArgMetArgThrIleThrPro 247
 746 GTTAACATGTGTAATTAATGAACGCCCTTCATGATGATGATGCTTATTAATTTAAGT-- 802

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QY 248 SerLeuValAspGluLeuLysAlaSerAsnProAspPheProGlu----- 262
Db 803 -----GATATTCTCGAAAGCAATCTGTAAGA 829
QY 263 -----ValSerSerGlyIleTyrValGlnGluValAlaProAsnSerProSer 278
Db 830 CTACACTACTCAATAAGCAAGCGCTTATGTAGCTAAAGTA-----GAC 874
QY 279 GlnArgGlyGlyIleGlnAspGlyAspIleIleValIleValAsnGlyArgProLeuVal 298
Db 875 AGTGAATAATGCCATTAAAGAGGTGATATTACTGAAATAGATGTAACAAATATAAA 934
QY 299 AspSerSerGluLeuGln 304
Db 935 GATGATACGATTTAAGA 952

RESULT 11
US-10-793-626-3756/c
; Sequence 3756, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3756
; LENGTH: 3650
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-3756

Alignment Scores:
Pred. No.: 7,81e-31 Length: 3650
Score: 347.00 Matches: 94
Percent Similarity: 50.94 Conservative: 72
Best Local Similarity: 28.88 Mismatches: 104
Query Match: 20.78 Indels: 56
DB: 8 Gaps: 11

US-10-617-443b-2 (1-334) x US-10-793-626-3756 (1-3650)
QY 8 SerAlaGlyLeuHisGlnLeuSerSerProArgTyrLysPheAsnPheIleAlaAspVal 27
Db 1304 AGTCATGCTGCAATCACTGATGATGTAAGTAATCAATCAATCACTGATGATGATG 1245
QY 28 ValGluLysIleAlaProAlaValAlaHisIle----- 38
Db 1244 ATTAAGACGTTTCTCCCGCAATTTCCGCGGATGAATAACGCAAAATCTACAAACCTT 1185
QY 39 --GluLeuPheLeuArgHisProLeuPheGlyArgAsnValProLeuSerSerGlySer 57
Db 1184 GATGATTTATTCACGCGTAAGCATCTAATCAAAAGAAAGCGGAATGTTCCGCTGCG 1125
QY 58 GlyPheIleMetSerGlu--AlaGlyLeuIleIleThrAsnAlaHisValAlaSerSer 76
Db 1124 ATTTATCAATAAGAGAGGTCCCGCATATTCGTTACAAATTAATCACGTTGTTAT-- 1068
QY 77 AsnSerAlaAlaProGlyArgGlnGlnLeuLysValGlnLeuGlnAsnGlyAspSerTyr 96
Db 1067 -----GTTGCTTCGGAATTAAGTTCACTACATCAATTAATCAAAACAAGTA 1023
QY 97 GluAlaThrIleLysAspIleAspLysLysSerAspIleAlaThrIleLysIleHisPro 116
Db 1022 GATGCCAATTAATTAAGTAAGACGCCCTCAACAGATATTGCTGTTCAAAATAAAGAT 963

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QY 117 LysIleLysLeuProValLeuLeuLeuGlyHisSerAlaAspLeuArgProGlyGluPhe 136
Db 962 ACAAGAGAAATTAAGCAATTCATTAATTCCTTAATTCGTAAGAGTCAACAGAGAGTACT 903
QY 137 ValValAlaIleGlySerProPheAlaLeuGln-----AsnThrValThrThrGlyIle 154
Db 902 GTTTTTCGAATGGGTAATCCTCTAGATTAAGATTGCAAAATTCGTTACATCAAGAAATT 843
QY 155 ValSerThrAlaGlnArgGlu--GlyArgGluLeuGlyLeuArgAspSerAspMetAsp 173
Db 842 ATTTCAGCTAGCGAAGCTACATTAATGACCCCAATCTTCCTGCTGTAATTAATTAAT 783
QY 174 TyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyProLeuValAsnLeu 193
Db 782 GTTTACAGACAGCGCTGCAATTAATCCGGTAATTCGGGTGTCATTTAGTGGAATATT 723
QY 194 AspGlyGluValIleGlyIleAsnThrLeuLysValThrAla-----GlyIle 209
Db 722 AACGGAATTCCTGTTGATCAATTCATGAATAATGGGCGACGACAGTGAAGTATTA 663
QY 210 SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGln 229
Db 662 GTTTTTCCTAATCCTAGTAATGAAGTTAGAGTGAACATC-----GAAACAATCTC 615
QY 230 IleLysAspTyrLys-----LysArgPheIleGlyIleArgMetArgThrIleThrPro 247
Db 614 GTTAAACATGTGTAATGAAGCCCTTCATTCGTTAATGCTTAAATTAATTAAGT--- 558
QY 248 SerLeuValAspGluLeuLysAlaSerAsnProAspPheProGlu----- 262
Db 557 -----GATATTCTCGAAAGCAATCTGTAAGA 531
QY 263 -----ValSerSerGlyIleTyrValGlnGluValAlaProAsnSerProSer 278
Db 530 CTACACTACTCAATAAGCAAGCGCTTATGTAGCTAAAGTA-----GAC 486
QY 279 GlnArgGlyGlyIleGlnAspGlyAspIleIleValLysValAsnGlyArgProLeuVal 298
Db 485 AGTGAATAATGCCATTAAAGAGGTGATATTACTGAAATAGATGTAACAAATATAAA 426
QY 299 AspSerSerGluLeuGln 304
Db 425 GATGATACGATTTAAGA 408

RESULT 12
US-11-074-176-3
; Sequence 3, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klienhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAniff, Olivia
; APPLICANT: Perill, Andrea Accarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Screens-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Lactobacillus acidophilus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1269)
; NAME/KEY: misc_feature

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; LOCATION: (0)...(0)
; OTHER INFORMATION: ORF 83; Serine protease HTRA
US-11-074-176-3

Alignment Scores:
Pred. No.: 4,88e-30 Length: 1269
Score: 335.50 Matches: 95
Percent Similarity: 48.1% Conservative: 54
Best Local Similarity: 30.6% Mismatches: 114
Query Match: 20.0% Indels: 47
DB: 12 Gaps: 11

US-10-617-443b-2 (1-334) x US-11-074-176-3 (1-1269)

QY 48 GYAAGAsnValProleuSerSerGlyPheIleMetSerGluA----- 64
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 397 GGCAGCTTGAGACTTACAGTGAAGTTCCAGTGTATTATATGAAGCAATGTGTA 456
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 65 GlyLeuIleIleThrAsnAlaHisValSerSerAsnSerAlaAlaProGlyArgGln 84
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 457 GGTATATTGTACTATATATACGTTATTTCAGCGAGATGCA----- 501
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 85 GlnLeuValGlnLeuGlnAsnGlyAspSerGlyAlaAlaThrIleLeuAspIleAsp 104
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 502 --GTTCAAGTGCACCTGCTTAATGCGACAGACTGTTAGTCGCAAGTTGTGGAAAGAT 558
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 105 LysLeuSerAspIleAlaThrIleLysIleHisProLysLysLeuProValLeuLeu 124
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 559 AGTACTACTGACTTACGTTTATATCAATGACGTAAAGTAAACACAAACAGCCGAA 618
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 125 LeuGlyHisSerAlaAspLeuArgProGlyGluPheValAlaIleGlySerProPhe 144
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 619 TTTCGGCATCTTAAGACTCTTCAAGCTGTCACAACTGTAATCTCTGAGGTTACCACTT 678
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 145 AlaLeuGln-----AenthrValThrThrGlyIleValSerThrAlaGlnArg----- 160
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 679 GGTATGCAATATGCTTCTACGCTAACGCCAGATATTATACAGCAGCGCTAGAACATATC 738
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 161 -----GluGlyArgGluLeuGlyLeuArgAspSerAspMetAspTrpIleGlnThr 177
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 739 TCAACTTCATCTGGTATATCAG-----CAACAGTTATTTCACAA 777
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 178 AspAlaIleIleAsnTrpGlyAsnSerGlyGlyProLeuValAsnLeuAspGlyGluVal 197
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 778 GATGACCCCACTTAACCCAGATTACTCAGTGTCATCTGTTACTCAGCTGGTCAAGTT 837
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 198 IleGlyIleAsnThrLeuLysVal-----ThrAlaGlyIle 209
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 838 ATCGGTATTATCTATGAGCTTCTCAATCAAGTATGATGCTTCTGTAGAAAGTATG 897
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 210 SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGln 229
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 898 GGAATTTGATCTTCGATGAAGAGTTGTAATCTGTAATGAATG----- 945
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 230 IleLysAspTrpLys-----LysArgPheIleGlyIleArg-----MetArgThr 244
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 946 GTTAAAGAGGGAATGATTAAGTCTGTCACAACTGGTGTAGAGTATGCTCTTGAAGGT 1005
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 245 IleThrProSerLeuValAspGlyLeuLysAlaSerAsnProAspPheProGluValSer 264
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1006 ATTCCTGAAGCATACAGAAAGTCGCTTAAGATTAAGTCA-----AACCTTAAG 1053
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 265 SerGlyIleTrpValGlnGluValAlaProAsnSerProSerGlnArgGlyIleGln 284
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1054 AGTGTATCTATGTTGCTTCAATTAATAAGATTAATTCAGCGCAAAATGACGAGCATGAAG 1113
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 285 AspGlyAspIleIleValLysValAsnGlyArgProLeuValAspSerSerGlyLeuGln 304
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1114 AGCGGTGATGTCATTAAGTGAAGTGAAGCAAGAAAGTGTGATGATGATGATCAATTAAC 1173
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 305 GluAlaValLeuThrGlu-----SerProLeuLeuGluValAlaArgGlyLys 321
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1174 AGTATCTTTACAGTCACAAAGTGTGTGACACTGTGAACATTAATTAATGAAGATGT 1233

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QY 322 AspAspLeuLeuPheSerIleAlaProGlu 331
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1234 AGAATGTCAACTTAAGTAAAGTAACTTGAA 1263

RESULT 13
US-10-793-626-1823
; Sequence 1823, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1823
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-793-626-1823

Alignment Scores:
Pred. No.: 4.37e-28 Length: 954
Score: 318.00 Matches: 86
Percent Similarity: 53.0% Conservative: 57
Best Local Similarity: 31.9% Mismatches: 79
Query Match: 18.9% Indels: 48
DB: 8 Gaps: 11

US-10-617-443b-2 (1-334) x US-10-793-626-1823 (1-954)

QY 56 GlySerGlyPheIle-----MetSerGlu--AlaGlyLeuIleIleThrAsnAlaHis 72
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 79 GGTTCGGTGTGATTTATCAAAATTAAGTAGAGGTTCCGATATATCTGTTCAAAATATATC 138
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 73 ValValSerSerAsnSerAlaAlaProGlyArgGlnGlnLeuLysValGlnLeuGlnAsn 92
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 139 GTTGTGTAT-----GCTGCTTCGGAATTAAGTTCACTACATAT 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 93 GlyAspSerGlyAlaAlaThrIleLysAspIleAspLysLysSerAspIleAlaThrIle 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 TCAAAACAAAGTATGATCCAAATTAAGTAAAGACGCCCTTAACAGATATGCTGTTCTA 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 113 LysIleHisProLysLysLeuProValLeuLeuLeuGlyHisSerAlaAspLeuArg 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 241 AAAATTAAGATTAACAAAGAAATTAAGCAATTAATTTGCTAATTCGTCAAAAGTTCA 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 133 ProGlyGluPheValAlaIleIleGlySerProPheAlaLeuGln-----AenthrVal 150
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 301 ACAGAGATATGATTTTTCGATATGATATCCCTAGATTAAGAAATTCGCAATTCCTGT 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 151 ThrThrGlyIleValSerThrAlaGlnArgGlu--GlyArgGluLeuGlyLeuArgAsp 169
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 361 ACATCAGAAATTAATTCAGCTAGCGAAAGTACAAATTAAGCCCAATTAATTCCTGCTGAT 420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 170 SerAspMetAspTrpIleGlnThrAspAlaIleIleAsnTrpGlyAsnSerGlyGlyPro 189
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 421 ACTTAAGTATATGTTTATACAGACAGACGCTGCAATTAATTCGCGTATTCGCGGTGTGCA 480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 190 LeuValAsnLeuAspGlyGluValIleGlyIleAsnThrLeuLysValThrAla----- 207
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 481 TTAGTGAATTAACGGAATCTCGTTGATCAATTCCTAGTAAGAAATTCGGGAGACAGCAA 540
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 208 -----GlyLysSerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPhe 225
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 541 GTAGAAAGTATTAAGTTTGTCTATTAACCTAGTAATGAAGTTAGATGACATC----- 591

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QY 226 GlnAspLySGlnIleLysAspTrpLys-----LysArgPheIleGlyIleArgMetArg 243
DB 592 ---GAACCACTGCTTAACATGATGAATTCGAACGCCCTTCAATGATGATATAGTCTTATA 648
QY 244 ThrIleThrProSerLeuValAspGluLeuLysAlaSerAspProAspPheProGlu--- 262
DB 649 AATTAACT-----GATATTCCTGAAAAC 672
QY 263 -----ValSerSerGlyIleTyrrValGlnGluValAlaPro 274
DB 673 TATCGTAAAGAACTACTACTCATTAAGACAAAGCGCTTATGATGACTAAAGTA----- 726
QY 275 AsnSerProSerGlnArgGlyGlyIleGlnAspGlyAspIleIleValLysValAsnGly 294
DB 727 -----GACAGTGAAGAAATGCCATTAAGAAAGGTGATATTAATTAAGTAAGATGATGAT 777
QY 295 ArgProLeuValAspSerSerGluLeuGln 304
DB 778 AAACAAATTAAGATGATACAGATTAAAGA 807

RESULT 14
US-10-750-185-32084
; Sequence 32084, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32084
; LENGTH: 908
; TYPE: DNA
; ORGANISM: Bovine 19866881917166
US-10-750-185-32084

Alignment Scores:
Pred. No.: 9 02e-24 Length: 908
Score: 282.00 Matches: 56
Percent Similarity: 95.3% Conservative: 5
Best Local Similarity: 87.5% Mismatches: 3
Query Match: 16.8% Indels: 0
Gaps: 0
DB: 8

US-10-617-443b-2 (1-334) x US-10-750-185-32084 (1-908)
QY 119 LysLeuProValLeuLeuLeuGlyHisSerAlaAspLeuArgProGlyGluPheValVal 138
DB 438 AAGCTGCTGTGCTACTGCTGCGCTCTCGAGAGCTGCGGCGGAGAGTTCTGTGCTC 497
QY 139 AlaIleGlySerProPheAlaLeuGlnAenThrValThrThGlyIleValSerThrAla 158
DB 498 GCCATTGGAAGCCCTTTTCCCTTCAAAAACGGTCAACACGGGATCGTCGACACACC 557
QY 159 GlnArgGluGlyArgGluLeuGlyLeuArgAspSerAspMetAspTyrrIleGlnThrAsp 178
DB 558 CAGCGTGTGGCAAGAACTGGGGCTCCGGAATCGGACATGACTACATCCAGACAGAC 617
QY 179 AlaIleIleAsn 182
DB 618 GCCATCATCAAC 629
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RESULT 15
US-10-750-623-32084
; Sequence 32084, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32084
; LENGTH: 908
; TYPE: DNA
; ORGANISM: Bovine 19866881917166
US-10-750-623-32084

Alignment Scores:
Pred. No.: 9 02e-24 Length: 908
Score: 282.00 Matches: 56
Percent Similarity: 95.3% Conservative: 5
Best Local Similarity: 87.5% Mismatches: 3
Query Match: 16.8% Indels: 0
Gaps: 0
DB: 8

US-10-617-443b-2 (1-334) x US-10-750-623-32084 (1-908)
QY 119 LysLeuProValLeuLeuLeuGlyHisSerAlaAspLeuArgProGlyGluPheValVal 138
DB 438 AAGCTGCTGTGCTACTGCTGCGCTCTCGAGAGCTGCGGCGGAGAGTTCTGTGCTC 497
QY 139 AlaIleGlySerProPheAlaLeuGlnAenThrValThrThGlyIleValSerThrAla 158
DB 498 GCCATTGGAAGCCCTTTTCCCTTCAAAAACGGTCAACACGGGATCGTCGACACACC 557
QY 159 GlnArgGluGlyArgGluLeuGlyLeuArgAspSerAspMetAspTyrrIleGlnThrAsp 178
DB 558 CAGCGTGTGGCAAGAACTGGGGCTCCGGAATCGGACATGACTACATCCAGACAGAC 617
QY 179 AlaIleIleAsn 182
DB 618 GCCATCATCAAC 629

Search completed: February 21, 2006, 23:01:29
Job time : 937 secs
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